



Db 943 nMetLysLysLysPheCysValLeuLysLysLysLysLeuSerGluAlaLysGluIleLysSe 963  
QY 3169 ACAGTTAGAGAAACAAAGCTAAATGGGACAGAGCTCTCAGTGTGAGATTGCCTTT 3228  
Db 963 rGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLe 983  
QY 3229 AAATCAAGAAAGAGAGAGAAAGAAATGTCGATATATTAAAAGAAAAAATTAGACCC-- 3286  
Db 983 uAsnGlnGluGluLysLysArgGlnAlaAspIleLeuAsnGluLysIleArgGluCl 1003  
QY 3287 -----GAGAGCAACTTAGGAAAAAGTTAGAGTGAACACCACTTGAACA 3333  
Db 1003 uLeuGlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluCl 1023  
QY 3334 GACTCTCAGAAATCAAGATAGAAATTTGAAAGTGTAAACAGTAATTTGAATCAGGTTTC 3393  
Db 1023 nAlaLeuArgIleGluAspIleGluLysSerValGluSerAsnLeuAsnGlnValSe 1043  
QY 3394 TCACACTCATGAAGTGAAGTAAATCTCTTTCATGAAAAATTCATGTTGAAAAAGAAAT 3453  
Db 1043 rHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluI 1063  
QY 3454 TGCATGCTAAACCTGAGTACCCACTGAAACATCAACACCTGAGGTGAAGGAAATAA 3513  
Db 1063 eAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlnLysGluAsnLy 1083  
QY 3514 ATACTTTGAGGACATTAAAGATTTTACAGAAAGAAAGTGTGAACTTCAAAATGACCTAAA 3573  
Db 1083 sTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLy 1103  
QY 3574 ACTGAACACAGAAACAGTACAAACAGGCGCTCAGTATAGAGACGCTTAAAGTTCT 3633  
Db 1103 sLeuLysGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLe 1123  
QY 3634 GAGCGAGAGAACACGATGCTGACTTCTAAATTTGAAGGAA 3673  
Db 1123 uIleAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 1136

## RESULT 14

US-10-007-805-553  
; Sequence 553, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugui  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margarita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007,805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 553  
; LENGTH: 1013  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-007-805-553

Alignment Scores:  
Pred. No.: 2,96e-134 Length: 1013  
Score: 2374.00 Matches: 512  
Percent Similarity: 62.62% Conservativity: 61  
Best Local Similarity: 55.96% Mismatches: 126  
Query Match: 36.82% Indels: 216

DB: 13 Gaps: 9  
US-09-602-362E-26 (1-3673) x US-10-007-805-553 (1-1013)  
QY 1199 TTGAGGCTCAAAAGAAACATCTGAGAAATTTTCATGGCAGCAAAAGAAAGATCTAGG 1258  
Db 12 MetSerProAlaLysGluThrSerGluLysPheThrTrpAlaLysGlyArgProArg 31  
QY 1359 AAGATCATCATGGGAGGAGAAAGAAACATCTGTAAGACTGAATCCCTGGCAGGAGTAACA 1318  
Db 32 LysIleAlaTrpGluLysLysGluThrProValLysThrGlyCysAlaLysValThr 51  
QY 1319 CCTAATAAACTGAAGTTTGGAAAAAGGAACATCTTAATATGATTCATCTCTCAACAAA 1378  
Db 52 SerAsnLysThrLysValLeuLysGlyArgSerLysMetIleAlaCysProThrLys 71  
QY 1379 GAAACATCTACAAAGCAAGTACAAATGTGGATGTGAGTTCTGTAGAGCCTATATCAGT 1438  
Db 72 GluSerSerThrLysAlaSerAlaAsn----- 80  
QY 1439 CTTTTCGCACACGCACTATTGAAAAATTCACAGTGTACAAAAAGTTGAGGAAGACTTTAAT 1498  
Db 80 ----- 80  
QY 1499 CTTGCTACCAAGATTATCTCTAAGAGTGTGCACAGAATTATACGTGTTTACCTGATGCT 1558  
Db 80 ----- 80  
QY 1559 ACATATCAAAAAGATATCAAAAACAATAAATACAAAAATAGAGATCAGATGTTCCCATCA 1618  
Db 81 -----AspGlnArgPheProSer 85  
QY 1619 GAATCCAAACGAGAGGAGATGAAGAATATCTTGGGATTCGGGAGTCTCTTTGAGAGT 1678  
Db 87 GluSerLysGlnGluAspGluGluTyrSerCysAspSerArgSerLeuPheGluSer 106  
QY 1679 TCTGCAAGACTCAAGTGTCTATACCTGAGTCTATGATCAGAAAGTAAATGAGAGATAAT 1738  
Db 107 SerAlaLysIleGlnValCysIleProGluSerIleTyrGlnLysValMetGluIleAsn 126  
QY 1739 AGAGAGTAGAGAGCTTCTCTGAGAGGCCATCTGCTTCAAGCCTCGCTNGAAATGCCAA 1798  
Db 127 ArgGluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGln 146  
QY 1799 AAGACTGTTCCAAATAAAGCCTTTGAATGCAAGAAATGAACAAACATGAGAGAGCTCAG 1858  
Db 147 AsnSerValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAspPro 166  
QY 1859 ATGTTCCCATCAGAATCCAAACAAAGAGCGATCAAGAAAAATCTTGGGATTCGAGAGT 1918  
Db 167 MetPheProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSer 186  
QY 1919 CCCTGTGAGACGGTTTCACAGAGGATGTGTATTTACCCAAAGCTACACATCAAAAGAA 1978  
Db 187 LeuCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGlu 206  
QY 1979 TTGATACCTTAAAGTGGAAAAATTAGAAGAGTCTCTGTTAAAGATGCTCTCTGGAAGCCT 2038  
Db 207 IleAspLysIleAsnGlyLysLeuGluGluSerProAsnLysAspGlyLeuLeuLysAla 226  
QY 2039 ACCTGTGGAAGAAAGTTCTCTTCCAAATAAAGCCTTAGAATTAAGACAGACAGAAACA 2098  
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QY 2099 TTCAAAGCAGAGTCTCTGATTAAGATGGTCTTCTGAGCCTACCTGTGGAAGGAAGTT 2158  
Db 247 PheLysAlaGluProGlyLysProSerAlaPheGluProAlaThrGluMetGlnLys 266  
QY 2159 TCTCTTCCAAATAAAGCCTTTAGAAATTAAGGACAGAGAAACACTCAAGCAGAGCTCTCT 2218  
Db 267 SerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAsp----- 284  
QY 2219 GATAATGATGCTCTCTGAGAGCCTACTCTGAGGAGAAAGTTCTCTTCCCAATAAAGCT 2278

Db 284 ----- 284  
QY 2279 TTAGAAATTGAGGACAGAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGATCCAAA 2338  
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QY 2339 CAAAAGGATGATGAAGAAATCTTTGGGATTTTGAGAGTTTCTTGAGACTCTCTTACAG 2398  
Db 293 GlnLysAspTyrGluGluAsnSerTrpAspThrGluSerLeuGluGluThrValSerGln 312  
QY 2399 AATGATGTGTGTTTCCCAAGCTCACATCAAAAAGAAATTCGATACCTTAAGTGGAAAA 2458  
Db 313 LysAspValCysLeuProLysAlaAlaHisGlnLysGluLeuAspLysIleAsnGlnLys 332  
QY 2459 TTAGAGAGTCTCCTGATAAAGATGCTCTTGAAGCCTTACCTGGGAATGAAATTTCT 2518  
Db 333 LeuGluGlySerProGlyLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSer 352  
QY 2519 CTTCCAAATTAAGCCCTTAGAATTTGAAGGACAGAGAAACATTCAAAAGCAGAGATGTGAGT 2578  
Db 353 IleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGluProGlu 372  
QY 2579 TCTGTAGAGTCCACATTCAGTCTTTTGGCAACCGACTACTGAAAATTCACAGTCTACA 2638  
Db 373 Lys---ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal 387  
QY 2639 AAAGTTGAGGAAGACTTTAATCTTACTACCAAGGAGGAGCAACAAAGACAGACTAAGTGA 2698  
Db 388 -----ProAsnLysAlaLeuGluLeu 394  
QY 2699 CAACAGGAACGTGATATTGGCATTATTGAACAGCTCCCAAGATCAACAAATAAGATG 2758  
Db 395 LysAsnGluGlnThrLeuArgAlaAspGluIleLeuPro----- 407  
QY 2759 CCCACATCAGAAATTAGGAGAGAAAGAGATACAAATCAACTTCAGATTCTGAGATTATC 2818  
Db 408 -----SerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeu 425  
QY 2819 TCTGTGAGTGATACACAGAAATATAGTGTCTTACCTGAGGCTACATATCAAAAAGAAATA 2878  
Db 426 CysGluThrValSerGlnLysAspValCysLeuProLysAlaAlaHisGlnLysGluIle 445  
QY 2879 AAGACAAACAAATGGCAATAGAGAGTCT----- 2908  
Db 446 AspLysIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysSerPro 465  
QY 2908 ----- 2908  
Db 466 CysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPhe 485  
QY 2909 -----CCTGAAAAGCCTTCTCACTTTGAGCTCGCCACTGCAATGCAAACTCT 2956  
Db 486 LysAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSer 505  
QY 2957 GTTCCAAATAAGCCTTAGAATGAGAGATAAACAACATTCAGAGACA----- 3004  
Db 506 ValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPhe 525  
QY 3004 ----- 3004  
Db 526 ProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSerLeuArg 545  
QY 3004 ----- 3004  
Db 546 GluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAsp 565  
QY 3005 -----GATTCAACTACCTATCAAAATCTTGATGATCACTTCT 3043  
Db 566 LysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHis 585  
QY 3044 TCTTGTGAAGAGGAGGAGGAACTTAAAGATACTGCAACAAATTCACACAAATG 3103

Db 586 SerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMet 605  
QY 3104 GAACAATGAAAAATAGTTTCTGTACTACAAAGGAACTGTCAAGAGCGAAAGAAATA 3163  
Db 606 GluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIle 625  
QY 3164 AAATCACAGTTAGAGAACCAAAAGCTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTG 3223  
Db 626 LysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLeuLeuCysSerValArgLeu 645  
QY 3224 CCTTAAATCAAGAGAGAGAGAGAAATGTCGATATATTAAAGAAAAAATTAGA 3283  
Db 646 ThrLeuAsnGlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArg 665  
QY 3284 CCC-----GAAGAGCAACTTAGGAAAAAGTTAGAAAGTGAACCAACTT 3328  
Db 666 GluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeu 685  
QY 3329 GAACAGACTCTCAGATACAGATATAGATTGAAAAGTGTAAACAGTAATTTGAATCAG 3388  
Db 686 GluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGln 705  
QY 3389 GTTCTCACACTCATGAAGTGAATGATCTCTTTCATGAAATTCATGTTGAAAAAG 3448  
Db 706 ValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLys 725  
QY 3449 GAAATTCCTGCTTAAACTGGAAGTAGCCACACTGAAACATCAACACAGGTGAGGAA 3508  
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QY 3509 AATAAATACTTGGAGCATTAAAGATTTTCAAGAAAAAGAAATGCTGAACCTTCAATGACC 3568  
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QY 3629 GTTCTGAGCGAGAGACAGATGCTGACTCTTAATTTGAAGAA 3673  
Db 786 ValLeuIleAlaGluAenThrMetLeuThrSerLysLeuLysGlu 800

## RESULT 15

US-10-076-622-553  
; Sequence 553 Application US/10076622  
; Publication No. US20030023036A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Persing, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C11  
; CURRENT APPLICATION NUMBER: US/10/076.622  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 553  
; LENGTH: 1013  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-076-622-553

Alignment Scores:  
Pred. No.: 2,96e-134 Length: 1013  
Score: 2374.00 Matches: 512  
Percent Similarity: 62.62% Conservative: 61  
Best Local Similarity: 55.96% Mismatches: 126  
Query Match: 36.82% Indels: 216  
DB: 14 Gaps: 9

US-09-602-362E-26 (1-3673) x US-10-076-622-553 (1-1013)



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Db      606 GluGlnMetLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIle 625
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Db      626 LysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeu 645
QY      3224 CCTTTAAATCAAGAAAGAGAGAGAAATGTCGATATATTAAAAAGAAAAAATTAGA 3283
Db      646 ThrLeuAsnGlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArg 665
QY      3284 CCC-----GAGAGCAACTTAGGAAAAAGTTAGAGTGAACACCAACTT 3328
Db      666 GluGluLeuGlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnGlnLeu 685
QY      3329 GAACAGACTCTCAGATACAGATATAGAAATGAAAAGTGTAAACAAGTAATTTGAATCAG 3388
Db      686 GluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGln 705
QY      3389 GTTCTCAGACTCATGAAAGTCAAAATGATCTCTTTTCATGAAAATTGCATGTTGAAAAAG 3448
Db      706 ValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLys 725
QY      3449 GAAATGCGCATCTAAAGTGAAGTAGCCACACTGAACATCAACACACAGTGAAGGAA 3508
Db      726 GluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGlu 745
QY      3509 AATAAATACTTTGAGCACATTAAAGATTTTCAAGAAAAAGAAATGCTGAACCTTCAAAATGACC 3568
Db      746 AsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThr 765
QY      3569 CTAAGACTGAACAGAAACAGATACAAAAGGGCATCTCAGTATAGAGAGCGCTTAAA 3628
Db      766 LeuLysLeuLysGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLys 785
QY      3629 GTTCTGACGCGAGAGAACACGATGCTGACTTCTAAATTGAAGGAA 3673
Db      786 ValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 800
```

Search completed: July 15, 2004, 09:47:29  
Job time : 321.903 secs

1. The first part of the document is a list of the names of the members of the committee.

2. The second part of the document is a list of the names of the members of the committee.

3.

4.

5. The third part of the document is a list of the names of the members of the committee.

6. The fourth part of the document is a list of the names of the members of the committee.

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: July 15, 2004, 08:36:32 ; Search time 158.061 Seconds

(without alignments)  
13131.604 Million cell updates/sec

Title: US-09-602-362E-26

Perfect score: 6448  
Sequence: 1 caagagcttgccgtacaga.....tgacttttaattgaaggaa 3673

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=A Geneseq\_29Jan04  
-LCOPEXT=0  
-LIST=45  
-MODE=LOCAL  
-USER=US09602362  
-NC MAP  
-DEV TIMEOUT=120  
-FGAPEXT=7

Database :  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5938	92.1	1225	6	ABR47547 Breast ca
2	5173	80.2	1011	6	AAB84703 Amino aci
3	5173	80.2	1239	6	ABJ37789 Human tum
4	3458	53.6	1341	4	AAB84702 Amino aci
5	3458	53.6	1341	5	ABJ05537 Breast ca
6	3458	53.6	1341	6	ABJ37784 Human tum
7	3458	53.6	1341	6	ABR47548 Breast ca
8	3440	53.3	1349	6	ABJ37788 Human tum
9	2374	36.8	1013	6	ABJ37783 Human tum
10	2372.5	36.8	1095	4	Aau33357 Human bre

11	2372.5	36.8	1095	5	ABG78924	ABG78924 Human bre
12	2372.5	36.8	1095	6	ABJ37747	Abj37747 Human tum
13	2367	36.7	1002	4	Aau33351	Aau33351 Human bre
14	2367	36.7	1002	5	ABG78918	ABG78918 Human bre
15	2367	36.7	1002	6	ABJ37741	Abj37741 Human tum
16	2367	36.7	1002	8	ADE44427	Ade44427 Human bre
17	1776.5	27.6	661	6	ABJ37782	Abj37782 Human tum
18	1775	27.5	743	4	Aau33358	Aau33358 Human bre
19	1775	27.5	743	5	ABG78925	ABG78925 Human bre
20	1775	27.5	743	6	ABJ37748	Abj37748 Human tum
21	1769.5	27.4	650	4	AAB50263	Aab50263 Human bre
22	1769.5	27.4	650	4	AAG65983	Aag65983 B726P spl
23	1769.5	27.4	650	4	Aau33346	Aau33346 Human bre
24	1769.5	27.4	650	5	ABG78913	ABG78913 Human bre
25	1769.5	27.4	650	6	ABJ37736	Abj37736 Human tum
26	1769.5	27.4	650	8	ADE44421	Ade44421 Human bre
27	1542	23.9	512	4	AAB84701	Aab84701 Amino aci
28	1414.5	21.9	445	4	AAB50249	Aab50249 Human bre
29	1414.5	21.9	445	4	AAG65987	Aag65987 B726P spl
30	1414.5	21.9	445	4	Aau33350	Aau33350 Human bre
31	1414.5	21.9	445	5	ABG78917	ABG78917 Human bre
32	1414.5	21.9	445	6	ABJ37740	Abj37740 Human tum
33	1414.5	21.9	445	8	ADE44425	Ade44425 Human bre
34	1384	21.5	466	4	AAB50248	Aab50248 Human bre
35	1384	21.5	466	4	AAG65986	Aag65986 B726P spl
36	1384	21.5	466	4	Aau33349	Aau33349 Human bre
37	1384	21.5	466	5	ABG78916	ABG78916 Human bre
38	1384	21.5	466	6	ABJ37739	Abj37739 Human tum
39	1384	21.5	466	8	ADE44424	Ade44424 Human bre
40	1311	20.3	399	6	ABJ37785	Abj37785 Human tum
41	1298	20.1	399	6	ABJ37787	Abj37787 Human tum
42	1142.5	17.7	398	3	AAB07638	Aab07638 Amino aci
43	884.5	13.7	432	4	AAB50244	Aab50244 Human bre
44	884.5	13.7	432	4	AAG65982	Aag65982 B726P thi
45	884.5	13.7	432	4	Aau33345	Aau33345 Human bre

ALIGNMENTS

RESULT 1

ABR47547

ID ABR47547 standard; protein; 1225 AA.

XX

AC ABR47547;

XX

DT 12-JUN-2003 (first entry)

XX

DE Breast cancer associated protein sequence SEQ ID NO:332.

XX

KW Human; breast cancer; cytostatic; gene therapy.

XX

OS Homo sapiens.

XX

PN WC2003004989-A2.

XX

PD 16-JAN-2003.

XX

PF 21-JUN-2002; 2002WO-US019669.

XX

PR 21-JUN-2001; 2001US-0299887P.

XX

PR 27-JUN-2001; 2001US-0301572P.

XX

PR 18-JUN-2001; 2001US-0306501P.

XX

PR 25-SEP-2001; 2001US-0325002P.

XX

PR 05-MAR-2002; 2002US-0362585P.

XX

PR 14-MAY-2002; 2002US-0380391P.

XX

(WILL-) MILLENIUM PHARM INC.

XX

PI Lillie J, Ganavarapu M, Glatt K, Hoersch S, Kamatkar S, Meyers RE;

PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Mills GB;

XX Bast RC, Hortobagyi GN, Pusztai L, Meric P, Sahin A, Mills GB;

XX WFI; 2003-210381/20.

DR

DR N-PSDB; ACC50245.  
XX  
XX PT Breast cancer diagnosis or treatment by comparing the level of expression  
PT of a marker in a patient sample with that in the control non-breast  
PT cancer sample.

XX Claim 1; SEQ ID NO 332; 128pp; English.

XX The present invention describes a method for assessing whether a patient  
XX is afflicted with breast cancer. The method comprises comparing the level  
XX of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
XX ABR47386 to ABR47632) in a patient sample and the normal level of  
XX expression of the marker in a control non-breast cancer sample, where a  
XX significant increase in the level of expression of the marker in the  
XX patient sample and the normal level is an indication that the patient is  
XX afflicted with breast cancer. The breast cancer associated sequences from  
XX the present invention have cytostatic activities and can be used in gene  
XX therapy. The method is useful for diagnosing and treating breast cancer.  
XX N.B. The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1225 AA;

Alignment Scores:  
Pred. No.: 0 Length: 1225  
Score: 5938.00 Matches: 1159  
Percent Similarity: 99.57% Conservative: 1  
Best Local Similarity: 99.48% Mismatches: 4  
Query Match: 92.09% Indels: 1  
DB: 6 Gaps: 0

US-09-602-362E-26 (1-3673) x ABR47547 (1-1225)

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Db 1 MetLysArgLeuLeuAlaAlaAlaGlyLysGlyValArgGlyProGluProProAsnPro 20  
QY 241 TTCAGGACGGGTCTACACTGAGAGGACTACGGGACCATCTACTCTGGGACTGAGG 300  
Db 21 PheSerGluArgValThrGluLysAspThrGlyThrIleTyrPheGlyAspLeuGly 40  
QY 301 AAGATCCATACAGCTCCCTCCCGGGCCCAAGTCCAGAAGCTGGAGAAGATCACAGTAGG 360  
Db 41 LysIleHisThrAlaAlaSerArgGlyGlnValGlnLysLeuGluLysMetThrValGly 60  
QY 361 AAGAAGCCGCTCACTGCAACAAAGAGATATGAGAGAGAGGACTGCTACACTGGGCC 420  
Db 61 LysLysProValAsnLeuAsnLysArgAspMetLysLysArgThrAlaLeuHisThrAla 80  
QY 421 TGTGTCATAGGCGCATCANAGTAGTAACATTTCTGCTAGACAGAAAGTGCNGCTTAAT 480  
Db 81 CysValAsnGlyHisAlaGluValThrPheLeuValAspArgLysCysGlnLeuAsn 100  
QY 481 GTCCTTGATGGCGAAGGAGGACACTCTGATGAGAGCTTCAATATGCGAGAGGAGACT 540  
Db 101 ValLeuAspGlyGluGlyArgThrProLeuMetLysAlaLeuGlnCysGluArgGluAla 120  
QY 541 TTGTGCAATATTTCTCATAGATGCTGGTCTCATCTTAAATATGATGATGATGATGCA 600  
Db 121 -CysAlaAsnIleLeuIleAspAlaGlyAlaAspLeuAsnTyrValAspValThrGlyAs 140  
QY 601 CAGGCTCTCCATTATGCGCTTTATAGTGAGAAATTTATTAATGTTGGCAACACTGCTGC 660  
Db 140 nThrAlaLeuHisTyrAlaValTyrSerGluAsnLeuLeuMetValAlaThrLeuLeuSe 160  
QY 661 CTATGCTGAGTCATCGAGTGCACAAACAGGCTAGCTCACACCCCTTTTACTGGCCAT 720  
Db 160 rTyrGlyAlaValIleGluValGlnAsnLysAlaSerLeuThrProLeuLeuLeuAlaI 180  
QY 721 ACAGAAAGAACAGCAACACTGTGGAATTTTACTAAACAAAAATGCAAAATGCAACGC 780  
Db 180 eGlnLysArgSerLysGlnThrValGluPheLeuLeuThrLysAsnAlaAsnAlaAsnAl 200

QY 781 ATTAATAGCTCTAAATGACAGCCCTCATGCTTGCATATGTGAAGGCTCATCAGAGAT 840  
Db 200 aPheAsnGluSerLysCysThrAlaLeuMetLeuAlaIleCysGluGlySerSerGluI 220  
QY 841 AGTCGGCATCTTCTTCAGCAAAATGTTGCGTCTTTGCTGAGAGACATACATGATATAC 900  
Db 220 eValGlyMetLeuLeuGlnGlnAsnValAspValPheAlaGluAspIleHisGlyIle 240  
QY 901 TGCAAGAACGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Db 240 rAlaGluArgTyrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 260  
QY 961 TATACGAAATTAACCTTAAATAATCCTCAAAATCAATCAATCAATCAATCAATCAATCA 1020  
Db 260 sIleArgLysLeuProLysAsnProGlnAsnThrAsnProGluGlyThrSerThrGly 280  
QY 1021 ACCTGATGAGGCTGCACCTTGGCGGAAAGAACACCTGACACCGCTGAAAGCTTGCTGA 1080  
Db 280 rProAspGluAlaAlaProLeuAlaGluArgThrProAspThrAlaGluSerLeuLeu 300  
QY 1081 AAAAACACCTGACGAGGCTGCACCTTGGTGGAGGAAACGCTGTGCCAAAATCAATGCT 1140  
Db 300 uLysThrProAspGluAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 320  
QY 1141 GGGGAAAGCAACATCTGGAAGTTTGAACAGTCAACAGAGAAACACCTAGGAAATTTT 1200  
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QY 1201 GAGGCTTACAAAAGAAACATCTGAGAAATTTTCATGCCCAAGAAAGAAAGTCTAGGAA 1260  
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QY 1261 GATCACATGGAGGAAAGAAACATCTGTAAGACTGAATCGTGGCAGGATACAC 1320  
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QY 1321 TAATAAACTGAAAGTTTGGAAAAAGAACATCTAATATGATTGATGCTCTACAAAGA 1380  
Db 380 oAsnLysThrGluValLeuGluLysGlyThrSerAsnMetIleAlaCysProThrLys 400  
QY 1381 AACATCTACAAAAGCAAGTACAAATGTGGATGTGAGTCTGTAGAGCCCTATATTCAGT 1440  
Db 400 uThrSerThrLysAlaSerThrAsnValAspValSerSerValGluProIlePheSer 420  
QY 1441 TTTTGGCACACGACATTTGAAAATTCACAGTCTACAAAAGTTGAGCAAGACTTTAATCT 1500  
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QY 1501 TGCTACCAAGATTATCTTAAGAGTCTGCACAGAATTATAGCTGTTTACCTGATGCTAC 1560  
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QY 1681 TGCAAGACTCAAGTGTGTATACCTGAGTCTATGATATGATATGATATGATATGATATG 1740  
Db 500 rAlaLysThrGlnValCysIleProGluSerMetTyrGlnLysValMetGluIleAsn 520  
QY 1741 AGAAGTAGAAGAGACTCTCCTGAGAAAGCCTCTGCTTCAAGCCCTGCGCTGAAATGCAAAA 1800  
Db 520 gGluValGluGluLeuProGluLysProSerAlaPheLysProAlaIleGluMetGln 540  
QY 1801 GACTGTTCCAAATAAGCCCTTTGAATTTGAAGATGAACAAACATTTGAGAGCAGCTCAGAT 1860  
Db 540 sThrValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAlaGlnMe 560



1861 GTTCCCATCAGATCCAAACAAAGGACGATGAAGAAAATCTTGGGATTCAGAGTCC 1920  
Db tPheProSerGluSerLysGlnLysAspAspGluGluAsnSerTrpAspSerGluSerPr 580  
1921 CTGTGAGACGGTTTCACAGAGGATGTGTATTTACCCAAAGCTACACATCAAAAAGAAAT 1980  
Db oCysGluThrValSerGlnLysAspValLysLeuProLysAlaThrHisGlnLysGluPh 600  
1981 CGATACCTTAAGTGGAAAATAGAGAGTCCTCTGTTAAAGATGGTCTTCTGAGAGCTTAC 2040  
Db eAspThrLeuSerGlyLysLeuGluGluSerProValLysAspGlyLeuLeuLysProTh 620  
2041 CTGTGGAAGGAAAGTTCTCTTCCAAATAAAGCCCTTAGAATTAAGGACAGAGAAACATT 2100  
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2101 CAAGCAGAGTCTCTGTATAAGATGCTCTCTGAGCCTACCTGTCGGAAGGAAGTTTC 2160  
Db eLysAlaGluSerProAspLysAspGlyLeuLeuLysProThrCysGlyArgLysValSe 660  
2161 TCTTCCAAATAAAGCCTTAGAATTAAGGACAGAGAAACACTCAAGCAGAGTCTCTCTGA 2220  
Db rLeuProAsnLysAlaLeuGluLeuLysAspArgGluThrLeuLysAlaGluSerProAs 680  
2221 TAATGATGGTCTCTGAAGCCTACCTGTGGAAGGAAGTTCTCTTCCAAATAAAGCTTT 2280  
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2281 AGAATTGAAGACAGAGAAACATTCAAGCAGCTCAGATGTTCCCATCAGAAATCCAAACA 2340  
Db uGluLeuLysAspArgGluThrPheLysAlaAlaGlnMetPheProSerGluSerLysGl 720  
2341 AAAGATGATGAAGAAAATCTCTGGGATTTTGAGAGTTTCTCTGAGACTCTCTTACAGAA 2400  
Db nLysAspAspGluGluAsnSerTrpAspPheGluSerPheLeuGluThrLeuLeuGlnAs 740  
2401 TGATGTGTGTTTACCAAGGCTACACATCAAAAGAAATTCGATACCTTAAGTGGAATTT 2460  
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2461 AGAAGACTCTCTGTATAAGATGGTCTCTCTGAAGCCTACCTGTGGAATGAAAATTTCTCT 2520  
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2521 TCCAAATAAAGCCTTAGAATTAAGGACAGAGAAACATTCAAGCAGAGGATGTGAGTTC 2580  
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2581 TGATAGTCCACATTGAGTCTTTTGGCAACCCGACTACTGAAAATTCACAGTCTACAAA 2640  
Db rValGluSerThrPheSerLeuPheGlyLysProThrThrGluAsnSerGlnSerThrLys 820  
2641 AGTGAGGAAGACTTTAATCTTTACTACCAAGGAGGAGCAACAAAGACAGTAATCTGACA 2700  
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2701 ACAGNAAGCTGTATTTGGCATTTTGAAGCCTCCACAGATCAACAAATATAGATGCC 2760  
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2761 CACATCAGAAATTAAGGAAGAAAGATACAAAATCAAACTTCTGAGATTCTGAGATTATCTC 2820  
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2821 TGTGAGTGATACACAGAAATATGAGTGTGTTTACTGAGGCTACATATCAAAAGAAATAAA 2880  
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2881 GACAAACAATGCAAAATAGAGAGTCTCTGAAAAGCCTTCTCACTTTGAGCCTGCCAC 2940  
Db sThrThrAsnGlyLysIleGluSerProGluLysProSerHisPheGluProAlaTh 920  
2941 TGAATTCGAAAATCTGTTTCCAAATAAAGCCTTAGAATGGAAGAAATAACAAACATTGAG 3000

920 rGluMetGlnAsnSerValProAsnLysGlyLeuGluThrLysAsnLysGlnThrLeuAr 940  
3001 AGCAGAGTCAACTACCTATCAAAAATCTTGATGACACTTCTCTTGTGAAAAGAGGAAG 3060  
Db gAlaAspSerThrThrLeuSerLysIleLeuAspAlaLeuProSerCysGluArgGlyAr 960  
3061 GGAACCTTAAAAAGATAACTGTGAACAAAATTTACAGCAAAAATGGAACAAAATAATAA 3120  
Db gGluLeuLysLysAspAsnCysGluGlnIleThrAlaLysMetGluGlnMetLysAsnLys 980  
3121 GTTTTGTGTACTACAAAGAACTGTCAAGCGGAAAGAAATAAATACACAGTACAGAA 3180  
Db sPheCysValLeuGlnLysGluLeuSerGluAlaLysGluIleLysSerGlnLeuGluAs 1000  
3181 CCAAAAAGCTTAAATGGAACCAAGCTCTGCACTGTGAGATTGCCCTTTAAATCAAGAAGA 3240  
Db nGlnLysAlaLysTrpGluGlnLysCysSerValArgLeuThrLeuAsnGlnGluGl 1020  
3241 AGAGAGAGAGAAATGTGATATATTAAGAAAATAAAGAAAATTAGACCCGAAGAGCAACTAG 3300  
Db uGluLysArgArgAsnValAspIleLeuLysGluLysIleArgProGluGluGlnLeuAr 1040  
3301 GAAAAAGTTAGAAAGTGAACCAACTTGAACAGACTCTCAGAAATACAAAGATATAGAATT 3360  
Db gLysLysLeuGluValLysGlnGlnLeuGluGlnThrLeuArgIleGlnAspIleGluLe 1060  
3361 GAAAACTGTAAACAAGTAATTTGAATCAGGTTTCTCACTCATGAAAGTGAATAATGATCT 3420  
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3421 CTTCATGAAAATTTGATGTTTGAAGGAAATTAATAATCTTGAGGACATTAAGATTTTACA 3480  
Db uPheHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluValAlaTh 1100  
3481 ACTGAAACATCAACACAGCTGAAGGAAATTAATAATCTTGAGGACATTAAGATTTTACA 3540  
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3541 AGAAAAGATGCTGAACCTTCAAAATGACCTTAAACTGAAACAGAAAACAGTACAAAAG 3600  
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3601 GGCACTCTCAGTATAGAGCAGCTTAAAGTTCTGAGCGGAGAGAAACCAATGCTGACTTC 3660  
Db gAlaSerGlnTyrArgGluGlnLeuLysValLeuThrAlaGluAsnThrMetLeuThrSe 1160  
3661 TAAATTGAAGGAA 3673  
Db rLysLeuLysGlu 1164

## RESULT 2

AAB84703  
ID AAB84703 standard; protein; 1011 AA.

XX AC AAB84703;

XX AC 17-SEP-2001 (first entry)

XX DE Amino acid sequence of a human cancer associated antigen.

XX DE Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine.

XX OS Homo sapiens.

XX PN WO200147959-A2.

XX PD 05-JUL-2001.

XX XX 29-NOV-2000; 2000WO-US042334.

XX XX 30-NOV-1999; 99US-00451739.

XX PR 24-OCT-2000; 2000US-00602362.

XX (LUDW-) LUDWIG INST CANCER RES.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 PA (CORR) CORNELL RES FOUND INC.  
 XX  
 XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;  
 XX WPI; 2001-441706/47.  
 XX  
 XX Isolated cancer associated nucleic acid molecule identified by SEREX  
 PT (serological identification of antigens by recombinant expression  
 PT cloning) technique, useful in nucleic acid based therapies to treat  
 PT cancer.  
 XX  
 XX Claim 83; Page 59-62; 62pp; English.  
 XX  
 CC The present sequence represents a human cancer associated antigen. The  
 CC sequence was identified using probes derived from the INGI gene. The INGI  
 CC gene is a tumour suppressor candidate gene. The cancer associated antigen  
 CC polynucleotides and polypeptides are useful for screening for the  
 CC possible presence of a pathological condition in a subject such as  
 CC cancer. The cancer associated antigen polypeptides are useful for  
 CC producing vaccines  
 XX  
 SQ Sequence 1011 AA;  
 Alignment Scores:  
 Pred. No.: 0 Length: 1011  
 Score: 5173.00 Matches: 1011  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.23% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-602-362E-26 (1-3673) x AAB84703 (1-1011)  
 QY 641 ATGGTGGCAACTGCTGCTCTATGGTCAGTCATCGAGGTGCAAAACAAAGCTAGCCCTC 700  
 DB 1 MetValAlaThrLeuLeuSerTyrGlyAlaValIleGluValGlnAsnLysAlaSerLeu 20  
 QY 701 ACACCCCTTTTACTGGCCATACAGAAAGCAAGCAAACTGTGGAATTTTACTAACA 760  
 DB 21 ThrProLeuLeuLeuAlaIleGlnLysArgSerLysGlnThrValGluPheLeuLeuThr 40  
 QY 761 AAAATGCAATGCAAAACGCTTTAATGAGTCTAAATGCAAGCCCTCATGCTTGCCATA 820  
 DB 41 LysAsnAlaAsnAlaPheAsnGluSerLysCysThrAlaLeuMetLeuAlaIle 60  
 QY 821 TGTGAGGCTCATCAGATAGTCTGCGATGCTTCTTCAGCAAAATGTTGAGTCTTTGCT 880  
 DB 61 CysGluGlySerSerGluIleValGlyMetLeuLeuGlnGlnAsnValAspValPheAla 80  
 QY 881 GAAGACATACATGGAATTAACCTGAGAAGCGTTATGCTGCTGCTGCGTGGAGTTAATTACATT 940  
 DB 81 GluAspIleHisGlyIleThrAlaGluArgTyrAlaAlaAlaArgGlyValAsnTyrIle 100  
 QY 941 CATCAACAACCTTTTGGACATATAGAAATTTACTTAAATCTCAAAATACCAATCCA 1000  
 DB 101 HisGlnGlnLeuLeuGluHisIleArgLysLeuProLysAsnProGlnAsnThrAsnPro 120  
 QY 1001 GAAGAACATCTACAGGAACACCTGATGAGGTGCGACCTTGGCGGAAAGAACACCTGCAC 1060  
 DB 121 GluGlyThrSerThrGlyThrProAspGluAlaAlaProLeuAlaGluArgThrProAsp 140  
 QY 1061 ACGGCTGAAGCTTCTGGAATAAACACCTGACGAGGCTGCACGCTTGGTGGAGGAACG 1120  
 DB 141 ThrAlaGluSerLeuLeuGluLysThrProAspGluAlaAlaArgLeuValGluGlyThr 160  
 QY 1121 TCTGCCAAATTCATGCTGGGGAAAGCAACATCTGGAAGTTTGAACAGTCAACAGAA 1180  
 DB 161 SerAlaLysIleGlnCysLeuGlyLysAlaThrSerGlyLysPheGluGlnSerThrGlu 180  
 QY 1181 GAAACACCTAGGAAATTTTGGAGGCTCAAAAGAAACATCTGAGAAATTTTCATGGCCA 1240

DB 181 GluThrProArgLysIleLeuArgProThrLysGluThrSerGluLysPheSerTrpPro 200  
 QY 1241 GCAAAGAAAGATCTAGGAAGATCACATGGAGGAGAAAGAAACATCTGTAAAGACTGAA 1300  
 DB 201 AlalysGluArgSerArgLysIleThrTrpGluGluLysGluThrSerValLysThrGlu 220  
 QY 1301 TGGTGCAGAGTAACACCTTAATAAAGTGAAGTTTGGAAAAGGACATCTATATG 1360  
 DB 221 CysValAlaGlyValThrProAsnLysThrGluValLeuGluLysGlyThrSerAsnMet 240  
 QY 1361 ATTGCATGCTCTACAAAAGAAACATCTACAAAAGCAAGTACAAATGTGATGTGACTTCT 1420  
 DB 241 IleAlaCysProThrLysGluThrSerThrLysAlaSerThrAsnValAspValSerSer 260  
 QY 1421 GTAGAGCTATATTCAGTCTTTTGGCACAGGACTATTGAAAATTCACAGTGTCAAAA 1480  
 DB 261 ValGluProIlePheSerLeuPheGlyThrArgThrIleGluAsnSerGlnCysThrLys 280  
 QY 1481 GTTGAGGAACACTTTAATCTTGTACCAAGATTATCTTAAGAGTGTCTGCACAGAATTAT 1540  
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 QY 1541 ACGTGTTCCTGATGCTACATATCAAAAAGATATCAAAACATAAATCACAAAATAGAA 1600  
 DB 301 ThrCysLeuProAspAlaThrTyrGlnLysAspIleLysThrIleAsnHisLysIleGlu 320  
 QY 1601 GATCAGATGTTCCATCAGAAATCCAAACGAGAGGAGATGAAGAAATATCTTGGGATCT 1660  
 DB 321 AspGlnMetPheProSerGluSerLysArgGluGluAspGluLysSerTrpAspSer 340  
 QY 1661 GGGAGTCTCTTTGAGAGTCTTGCAAAAGACTCAAGTGTGTATACCTGAGTCTATGTATCAG 1720  
 DB 341 GlySerLeuPheGluSerSerAlaLysThrGlnValCysIleProGluSerMetTyrGln 360  
 QY 1721 AAGTAAATGAGATAAATAGAGAGTAGAGAGCTTCTGAGAGGACATCTCCCTCAAG 1780  
 DB 361 LysValMetGluIleAsnArgGluValGluGluLeuProGluLysProSerAlaPheLys 380  
 QY 1781 CTGTGGCTGNAATGCAAAAGACTGTTCCAAATAAAGCCCTTGAATGAAGAAATCAACAA 1840  
 DB 381 ProAlaValGluMetGlnLysThrValProAsnLysAlaPheGluLeuLysAsnGluGln 400  
 QY 1841 ACATTGAGACAGCTCAGATGTTCCCATCAGAAATCCAAACAAAGAGCAGATGAAGAAAT 1900  
 DB 401 ThrLeuArgAlaAlaGlnMetPheProSerGluSerLysGlnLysAspGluGluAsn 420  
 QY 1901 TCTTGGATTCTCAGAGTCCCTGTGAGACGGTTTTCACAGAGGATGTGTATTACCCAAA 1960  
 DB 421 SerTrpAspSerGluSerProCysGluThrValSerGlnLysAspValTyrLeuProLys 440  
 QY 1961 GCTACACATCAAAAAGAAATTCGATACCTTAAGTGGAAATTAAGAGAGTCTCCTGTTAAA 2020  
 DB 441 AlaThrHisGlnLysGluPheAspThrLeuSerGlyLysLeuGluGluSerProValLys 460  
 QY 2021 GATGCTCTCTGAGGCTACCTGTGGAAGGAAAGTTTCTTCCAAATAAAGCCTTAGAA 2080  
 DB 461 AspGlyLeuLeuLysProThrCysGlyArgLysValSerLeuProAsnLysAlaLeuGlu 480  
 QY 2081 TTAAGGACAGAGAAACATTCAAAAGCAGAGTCTCTGTGATAAAGATGGTCTTCTGAAGCCT 2140  
 DB 481 LeuLysAspArgGluThrPheLysAlaGluSerProAspLysAspGlyLeuLeuLysPro 500  
 QY 2141 ACCTGTGGAGGAAAGTTTCTTCCAAATAAAGCCTTAGAATTAAGGACAGAGAAACA 2200  
 DB 501 ThrCysGlyArgLysValSerLeuProAsnLysAlaLeuGluLeuLysAspArgGluThr 520  
 QY 2201 CTCAAGACAGAGTCTCCTGATATATGATGTCTTCTGAAGCCTACCTGTGGAAGAAAGT 2260  
 DB 521 LeuLysAlaGluSerProAspAsnAspGlyLeuLeuLysProThrCysGlyArgLysVal 540  
 QY 2261 TCTCTCCAAATAAAGCTTTAGATTGAAGGACAGAGAAACATTCAAAGCAGCTCAGATG 2320

Db 541 SerLeuProAsnLysAlaLeuGluLeuLysAspArgGluThrPheLysAlaAlaGlnMet 560  
 QY 2321 TTCCATCAGAAATCCAAACAAAGAGATGATGAAGAAAATTTCTGGGATTTTGGAGTTTC 2380  
 Db 561 PheProSerGluSerLysGlnLysAspAspGluGluAsnSerTrpAspPheGluSerPhe 580  
 QY 2381 CTGAGACTCTCTTACAGAAATGATGTGTGTTTACCAAGGCTACACATCAAAAAGAAATTC 2440  
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 QY 2441 GATACCTTAAGTGGAAAAATTAGAGAGTCTCCTGATAAAGATGCTTCTTCAAGCCCTACC 2500  
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 QY 2501 TGTGGAATGAAAATTTCTCTTCCAAATAAGCCTTAGAATTGAAGCAGAGAAACATTC 2560  
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 QY 2561 AAAGCAGAGGATGTCAGTCTGTAGAGTCCACATTCAGTCTTTTGGCAACCCAGCTACT 2620  
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 QY 2741 GATCAACAAATAAGATGCCACATCAGAAATAGGAAGAAAGAGATACAAAATCAACT 2800  
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 QY 2801 TCAGATCTGAGATTATCTGTGATGATACACAGAAATATGATGTTTACCTGAGGCT 2860  
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 QY 3161 ATAAATACAGTTAGAACCAAAAAGCTAAATGGAAACAGAGCTCTGAGTGTGAGA 3220  
 Db 841 IleLysSerGlnLeuGluAsnGlnLysAlaLysTrpGluGlnGluCysSerValArg 860  
 QY 3221 TTGCCTTTAAATCAAGAAGAGAGAGAAATGTCATATATTAAGAAAAAATTT 3280  
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QY 3401 CATGAAGTGAATAATGATCTCTTCATGAATAATTCATGCTTTGAAAAGGAAATTCGCATG 3460  
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 QY 3521 GAGGACATTAAGATTTTACAAGAAAAGATGCTGAACCTCAAAATGACCTAAACTGAAA 3580  
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 QY 3641 GAGAACACAGTGTGACTTCTTAATTTGAAGGAA 3673  
 Db 1001 GluAsnThrMetLeuThrSerLysLeuLysGlu 1011  
 RESULT 3  
 ABU37789  
 ID ABU37789 standard; protein; 1239 AA.  
 XX AC ABU37789;  
 XX AC  
 XX 15-MAY-2003 (first entry)  
 DT  
 XX Human tumour-related protein - SEQ ID No 577.  
 DE  
 XX Human; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 KW tumour; breast cancer; cancer; immune response stimulation.  
 KW  
 XX Homo sapiens.  
 OS  
 XX W0200283956-A1.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 15-APR-2002; 2002WO-US012378.  
 PF  
 XX 13-APR-2001; 2001US-00834759.  
 PR 07-DEC-2001; 2001US-00007805.  
 PR 13-FEB-2002; 2002US-00076622.  
 XX  
 (CORI-) CORIXA CORP.  
 PA  
 XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 PI Mitcham JU, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;  
 PI Vedvick TS, McNeill PD, Durham M;  
 XX  
 WPI; 2003-103376/09.  
 XX  
 New polypeptide and polynucleotide useful for stimulating and/or  
 PT expanding T cells specific for a tumor protein and treating breast  
 PT cancer.  
 XX  
 Example 13; Page 359-363; 375pp; English.  
 PS  
 XX The invention comprises a method of stimulating and/or expanding T cells  
 CC specific for a tumour protein. The invention further comprises human  
 CC nuclear acids and proteins that are associated with tumours (e.g. breast  
 CC cancer). The method and sequences of the invention are useful for  
 CC stimulating and/or expanding T cells specific for a tumour protein,  
 CC detecting the presence of cancer, stimulating an immune response in a  
 CC patient and treating breast cancer. The present amino acid sequence  
 CC represents a human tumour-related protein  
 XX  
 SQ Sequence 1239 AA;  
 Alignment Scores:  
 Pred. No.: 0 Length: 1239

Score: 5173.00 Matches: 1011  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.23% Indels: 0  
 DB: 6 Gaps: 0

US-09-602-362E-26 (1-3673) x ABU37789 (1-1239)

QY 641 ATGGTGGCAACACTGCTGCTCTATGTCAGTGCATGAGGTGCAGAGCTCAGAGCTAGCCCTC 700  
 DB 1 MetValAlaThrLeuLeuSerThrGlyAlaValIleGluValGlnAsnLysAlaSerLeu 20  
 QY 701 ACACCCCTTTTACTGGCCATACAGAAAGAACAGCAAACTGTGGAATTTTACTAACA 760  
 DB 21 ThrProLeuLeuAlaIleGlnLysArgSerLysGlnThrValGluPheLeuLeuThr 40  
 QY 761 AAAATGCAATGCAACCCATTATAGTCTAAATGCACAGCCCTCATGCTGCCATA 820  
 DB 41 LysAsnAlaAsnAlaPheAsnGluSerLysCysThrAlaLeuMetLeuAlaIle 60  
 QY 821 TGTGAAGGCTCATCAGAGATAGTCGGCATGCTTCTTCAGCAAAATGCTTGACGCTTTTGT 880  
 DB 61 CysGluGlySerSerGluIleValGlyMetLeuLeuGlnAsnValAspValPheAla 80  
 QY 881 GAAGACATACATGGAATTAACCTGAGAACGTTATGCTGCTGCTGGAGTTAATTACATT 940  
 DB 81 GluAspIleGlyIleThrAlaGluArgTyrAlaAlaAlaArgGlyValAsnTyrIle 100  
 QY 941 CATCAACAACTTTTGGAAATATACGAAATTTACCTAAATATCCCTCAAAATACCAATCCA 1000  
 DB 101 HisGlnGlnLeuLeuGluHisIleArgLysLeuProLysAsnProGlnAsnThrAsnPro 120  
 QY 1001 GAAGAACATCTACAGAAACACTGATGAGGCTGCACCTTGGCGGAAAGAACACCTGCAC 1060  
 DB 121 GluGlyThrSerThrGlyThrProAspGluAlaAlaProLeuAlaGluArgThrProAsp 140  
 QY 1061 ACGGCTGAAAGCTTGTGGAATAAACACCTGACGAGGCTGCACGCTTGGTGGGGAACG 1120  
 DB 141 ThrAlaGluSerLeuLeuGluLysThrProAspGluAlaAlaArgLeuValGluGlyThr 160  
 QY 1121 TCTGCCAAATTCATGCTGGGGAAGCAACATCTGGAAGTTTGAACAGTCAACAGAA 1180  
 DB 161 SerAlaLysIleGlnCysLeuGlyLysAlaThrSerGlyLysPheGluGlnSerThrGlu 180  
 QY 1181 GAACACCTAGGAATTTTGGGCTCAAAAGAACATCTGAGAAATTTTCAAGGCCA 1240  
 DB 181 GluThrProArgLysIleLeuArgProThrLysGluThrSerGluLysPheSerThrPro 200  
 QY 1241 GCAAAAGAAAGATCAGGAAGATCAGCTGGGAGGAGAAAGAAACATCTGTAAGACTGAA 1300  
 DB 201 AlaLysGluArgSerArgLysIleThrTrpGluGluLysGluThrSerValLysThrGlu 220  
 QY 1301 TCCGTGGCGAGGTAAACCTTAATAAAGTAAAGTTTGGAAAAGGAAACATCTAATATG 1360  
 DB 221 CysValAlaGlyValThrProAsnLysThrGluValLeuGluLysGlyThrSerAsnMet 240  
 QY 1361 ATTGCATGCTCTACAAAAGAACATCTCAAAAGCAAGTACAAATGTGATGTCAGTTCT 1420  
 DB 241 IleAlaCysProThrLysGluThrSerThrLysAlaSerThrAsnValAspValSerSer 260  
 QY 1421 GPAGAGCTTAATTCAGTCTTTTGGCACAGGACTATTGAAATTCACAGTGTACAAA 1480  
 DB 261 ValGluProIlePheSerPheGlyThrArgThrIleGluAsnSerGlnCysThrLys 280  
 QY 1481 GTTGAAGGAGCTTAATTCCTGCTACCAAGATTATCTTAAGCTGTGCTGACACAAATTAT 1540  
 DB 281 ValGluGluAspPheAsnLeuAlaThrLysIleIleSerLysSerAlaAlaGlnAsnTyr 300  
 QY 1541 ACGTGTTCACCTGATGCTACATATCAAAAGATATCAAAACAATTAATCAAAATAGAA 1600  
 DB 301 ThrCysLeuProAspAlaThrTyrGlnLysAspIleLysThrIleAsnHisLysIleGlu 320  
 QY 1601 GATCAGATGTTCCCATCAGATCCAAACGAGGAGNAGATGAAGATATTCTTGGGATTC 1660

DB 321 AspGlnMetPheProSerGluSerLysArgGluGluAspGluGluThrSerTrpAspSer 340  
 QY 1661 GGGAGTCTCTTTGAGATCTTCGAAAGACTCAAGTGTGTATACCTGAGTCTTATGTATCAG 1720  
 DB 341 GlySerLeuPheGluSerSerAlaLysThrGlnValCysIleProGluSerMetTyrGln 360  
 QY 1721 AAAGTAATGAGATAAATAGAGAAGTAGAAGAGCTTCCTCAGAGCCATCTGCTCTCAAG 1780  
 DB 361 LysValMetGluLeuAsnArgGluValGluGluLeuProGluLysProSerAlaPheLys 380  
 QY 1781 CTGCTCCCTNGAAATGCAAAAGACTGTTCCAAATAAAGCCCTTGAATTGAAGATGAACAA 1840  
 DB 381 ProAlaValGluMetGlnLysThrValProAsnLysAlaPheGluLeuLysAsnGluGln 400  
 QY 1841 ACATTGAGACACGCTCAGATGTTCCCATCAGATCCAAACAAAGAGCAGATGAAGAAAT 1900  
 DB 401 ThrLeuArgAlaAlaGlnMetPheProSerGluSerLysGlnLysAspGluGluAsn 420  
 QY 1901 TCTTGGGATTTCTGAGAGTCCCTCTGAGACGTTTTCACAGAGGATGCTGATTTTACCCTCAA 1960  
 DB 421 SerTrpAspSerGluSerProCysGluThrValSerGlnLysAspValTyrLeuProLys 440  
 QY 1961 GCTACACATCAAAAGAAATTCGATACCTTAAGTGGAAATTTAGAAAGTCTCCTGTTAA 2020  
 DB 441 AlaThrHisGlnLysGluPheAspThrLeuSerGlyLysLeuGluGluSerProValLys 460  
 QY 2021 GATGGTCTTCTGAAGCCTACCTGTGGAAGGAAAGTTTCTTCCAAATAAAGCCTTAGAA 2080  
 DB 461 AspGlyLeuLeuLysProThrCysGlyArgLysValSerLeuProAsnLysAlaLeuGlu 480  
 QY 2081 TTAAGACACAGAAACATTCAAAGCAGAGTCTCTGATAAAGATGGTCTTCTGAAGCCT 2140  
 DB 481 LeuLysAspArgGluThrPheLysAlaGluSerProAspLysAspGlyLeuLeuLysPro 500  
 QY 2141 ACCTGTGGAAGGAAAGTTTCTTCTTCCAAATAAAGCCTTAGAATTTAAAGGACAGAGAAACA 2200  
 DB 501 ThrCysGlyArgLysValSerLeuProAsnLysAlaLeuGluLeuLysAspArgGluThr 520  
 QY 2201 CTCAAAGCAGAGTCTCTGATATGATGCTTCTTGAAGCCTACCTGTGGAAGGAAAGTT 2260  
 DB 521 LeuLysAlaGluSerProAspAsnAspGlyLeuLeuLysProThrCysGlyArgLysVal 540  
 QY 2261 TCTCTTCCAAATAAAGCCTTTAGNAATTGAAGGACAGAGAAACATTCAAAGCAGCTCAGATG 2320  
 DB 541 SerLeuProAsnLysAlaLeuGluLeuLysAspArgGluThrPheLysAlaAlaGlnMet 560  
 QY 2321 TTCCCATCAGAAATCCAAACAAAGGATGATGAAGAAATTTCTTGGGATTTTTCAGAGTTTC 2380  
 DB 561 PheProSerGluSerLysGlnLysAspAspGluGluAsnSerTrpAspPheGluSerPhe 580  
 QY 2381 CTGAGACTCTTTACAGAAATGATGTGCTTTTCCCAAGGCTACACATCAAAAGAAATTC 2440  
 DB 581 LeuGluThrLeuLeuGlnAsnAspValCysLeuProLysAlaThrHisGlnLysGluPhe 600  
 QY 2441 GATACCTTAAGTGGAAATTTAGAAAGTCTCTGATTAAGATGGTCTTCTGGAAGCTTACC 2500  
 DB 601 AspThrLeuSerGlyLysLeuGluGluSerProAspLysAspGlyLeuLeuLysProThr 620  
 QY 2501 TGTGGAATGAAATTTCTTCTTCCAAATAAAGCCTTAGAATTTGAAGACAGAGAAACATTC 2560  
 DB 621 CysGlyMetLysIleSerLeuProAsnLysAlaLeuGluLeuLysAspArgGluThrPhe 640  
 QY 2561 AAAGACAGAGATGTGAGTTCTGTAGATCCATTCAGTCTTCTTTTGGCAAAACCGACTACT 2620  
 DB 641 LysAlaGluAspValSerSerValGluSerThrPheSerLeuPheGlyLysProThrThr 660  
 QY 2621 GAAATTCACAGTCTCAAAAGTTCAGGAAGACTTTAATCTTACTACCAAGGAGGAGCA 2680  
 DB 661 GluAsnSerGlnSerThrLysValGluGluAspPheAsnLeuThrThrLysGluGlyAla 680  
 QY 2681 ACAGACAGATTAACGCAACAGCAAGCTGATATTTGGCATTTATGAACGAGCTCCACAA 2740

Db	691	ThrLysThrValThrGlyGlnGlnGluArgAspIleGlyIleIleGluArgAlaProGln	700
Qy	2741	GATCAACAAATAAGATGCCACATCAGAAATAGAGAACAAAGAGATACAAATCAACT	2800
Db	701	AspGlnThrAsnLysMetProThrSerGluLeuGlyArgLysGluAspThrLysSerThr	720
Qy	2801	TCAGATCTGAGATTATCTCTGTCAGTGATACACAGAAATATGAGTGTTCACCTGAGGCT	2860
Db	721	SerAspSerGluIleIleSerValSerAspThrGlnAsnTyrGluCysLeuProGluAla	740
Qy	2861	ACATATCAAAAGAAATAAAGACACAAATCGCAAAATAGAGAGTCTCTCGAAAGCCT	2920
Db	741	ThrTyrGlnLysGluIleLysThrThrAsnGlyLysIleGluGluSerProGluLysPro	760
Qy	2921	TCTCACTTTGAGCTGCCACTGAATGCAAACTCTGTTCCARATAAGGCTTAGAATGG	2980
Db	761	SerHisPheGluProAlaThrGluMetGlnAsnSerValProAsnLysGlyLeuGluTrp	780
Qy	2981	AAGAAATAACAAACATTCAGAGCAGATTCAACTACCTTATCAAAATCTTGGATGCACTT	3040
Db	781	LysAsnLysGlnThrLeuArgAlaAspSerThrThrLeuSerLysIleLeuAspAlaLeu	800
Qy	3041	CCTCTTTCTGAAAGAGGAGGAACCTTAAAAAGATAACTGTGAACAAATTTACAGCAAA	3100
Db	801	ProSerCysGluArgGlyArgGluLeuLysLysAspAsnCysGluGlnIleThrAlaLys	820
Qy	3101	ATGGACAAATCAGAAATAAGTTTGTCTACTACAAAGGAACTGTGAGAGCGAAAGAA	3160
Db	821	MetGluGlnMetLysAsnLysPheCysValLeuGlnLysGluLeuSerGluAlaLysGlu	840
Qy	3161	ATAAATCACAGTTAGAGACAAAGAACTAAATGGGAACAGAGCTCTGAGTGTGAGA	3220
Db	841	IleLysSerGlnLeuGluAsnGlnLysAlaLysTrpGluGlnGluLeuCysSerValArg	860
Qy	3221	TTGCCCTTTAAATCAGAGACAGAGAGAGAAATGTCGATATATTAAAGAGAAAATT	3280
Db	861	LeuProLeuAsnGlnGluGluLysArgArgAsnValAspIleLeuLysGluLysIle	880
Qy	3281	AGACCCGAGAGCAACTTAGGAAAAAGTTGAAGTGAAACACCACTTTGAACAGACTCTC	3340
Db	881	ArgProGluGlnGlnLeuArgLysLysLeuGluValLysHisGlnLeuGlnThrLeu	900
Qy	3341	AGATACAGATATAGATTGAAGTGTACAGTAATTTGAATCAGTTTCTCACACT	3400
Db	901	ArgIleGlnAspIleGluLysSerValThrSerAsnLeuAsnGlnValSerHisThr	920
Qy	3401	CATGAAAGTAAATGATCTCTTTTCATGAAATTCATGTTGAAAAAGCAAAATGCCCATG	3460
Db	921	HisGluSerGluAsnAspLeuPheHisGluAsnCysMetLeuLysLysGluIleAlaMet	940
Qy	3461	CTPAAACTGGAAGTAGCCACACTGAACATCAACACCAGGTGAGAGGAAAAATAACTTTT	3520
Db	941	LeuLysLeuGluValAlaThrLeuLysHisGlnHisGlnValLysGluAsnLysTyrPhe	960
Qy	3521	GAGGACATTAGATTTTACAGAAAGAGATGCTGAACCTCAATGACCTTAAACTGAAA	3580
Db	961	GluAspIleLysIleLeuGlnGlnLysAsnAlaGluLeuGlnMetThrLeuLysLeuLys	980
Qy	3581	CAGAAAAACAGTAACAAAAAGGCATCTCAGTAGTAGAGCAGCTTAAAGTTTCTGCGCA	3640
Db	981	GlnLysThrValThrLysArgAlaSerGlnTyrArgGluGlnLeuLysValLeuThrAla	1000
Qy	3641	GAGAACACAGTCTGACTTCTAAATTGAGGAA	3673
Db	1001	GluAsnThrMetLeuThrSerLysLeuLysGlu	1011
RESULT 4			
ID	AAB84702	standard; protein; 1341 AA.	
AC			
XX	AAB84702;		
XX			
DT	17-SEP-2001	(first entry)	

Amino acid sequence of a human cancer associated antigen.

Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine.

Homo sapiens.

WC200147959-A2.

05-JUL-2001.

29-NOV-2000; 2000WO-US042334.

30-NOV-1999; 99US-00451739.

24-OCT-2000; 2000US-00602362.

(LUDW-) LUDWIG INST CANCER RES.

(SLOK) SLOAN KETTERING INST CANCER RES.

(CORR) CORNELL RES FOUND INC.

Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;

WPI; 2001-441706/47.

Isolated cancer associated nucleic acid molecule identified by SEREX (serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat cancer.

Claim 83; Page 53-57; 62pp; English.

The present sequence represents a human cancer associated antigen. The sequence was identified using probes derived from the INGI gene. The INGI gene is a tumour suppressor candidate gene. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines

XX Sequence 1341 AA;

Alignment Scores:

Pred. No.:	2,38e-273	Length:	1341
Score:	3458.00	Matches:	740
Percent Similarity:	65.58%	Conservative:	83
Best Local Similarity:	58.96%	Mismatches:	159
Query Match:	53.63%	Indels:	273
DB:	4	Gaps:	12

US-09-602-362E-26 (1-3673) x AAB84702 (1-1341)

Qy	349	ATGACACTAGGGAAGAGCCGCTCAACCTGAACAAAGAGATATGAAGAGAGACTGCT	408
Db	1	MetThrLysArgLysLysThrIleAsnLeuAsnIleGlnAspAlaGlnLysArgThrAla	20
Qy	409	CTACACTGGCGCTGTGTCAATGGCCATGCGCANAAGTAGTAACATTTCTGTGTAGACAGAAAG	468
Db	21	LeuHisTrpAlaCysValAsnGlyHisGluGluValValThrPheLeuValAspArgLys	40
Qy	469	TGCNGCTTAATGTCCTTGATGGCGAAGGAGGACACCTCTGATGAGGCTTACATGTC	528
Db	41	CysGlnLeuAspValLeuAspGlyGluHisArgThrProLeuMetLysAlaLeuGlnCys	60
Qy	529	GAGAGGGAAGCTTTGTGCAATATTTCTCATAGATGCTGGTGGCTGATCTAAATTTATGTAGA	588
Db	61	HisGlnGluAla-CysAlaAsnIleLeuIleAspSerGlyAlaAspIleAsnLeuValAs	80
Qy	589	TGTGTATGGCAACACGGCTCTCCATTATGCCGTTTATGTAGAGAAATTTATATGTGTGGC	648
Db	80	pValTyrGlyAsnMetAlaLeuHisTyrAlaValTyrSerGluIleLeuSerValValAl	100
Qy	649	AACACTGCTGCTTATGTCGAGTCATCGAGGTGCAAAACAGGCTAGCCTCACACCCCT	708

100 aLysLeuLeuSerHisGlyAlaValIleGluValHisAsnLysAlaSerLeuThrProLe 120  
709 TTACTGGCCATACAGAAAGAGCAAGCAACTGTGGATTTTACTTAACAAAATGCG 768  
120 uLeuLeuSerIleThrLysArgSerGluGlnIleValGluPheLeuLeuIleLysAsnAl 140  
769 AAATGCAAAACGCAATTTAATGAGTCTAAATGCAAGCCCTCATGCTTGCATATGTGAAGG 828  
140 aAsnAlaAsnAlaValAsnLysIleThrLysCysThrAlaLeuMetLeuAlaValCysHisG 160  
829 CTATCAGAGATAGTGGGATGCTTCTTACGAAATGTGACGCTTTTGGTGAAGACAT 888  
160 ySerSerGluIleValGlyMetLeuLeuGlnAsnValAspValPheAlaAlaAspI 180  
889 ACATGCAATCACTGAGAGAGCTTATGCTGCTGCTGAGTGAATTAATCATCATCAACA 948  
180 eCysGlyValThrAlaGluHisTyrrAlaValThrCysGlyPheHisHisIleGluG 200  
949 ACTTTGGAAACATATACGAAATTTACCTAAATCTTCAAAATACCAATCCAGAGGAAC 1008  
200 nIleMetGluTyrrIleArgLysLeuSerLysAsnHisGlnAsnThrAsnProGluGly 220  
1009 ATCTACAGAAACACCTGATGAGGCTGACCCCTGGCGG----- 1045  
220 rSerAlaGlyThrProAspGluAlaAlaProLeuAlaGluArgThrProAspThrAlaG 240  
1046 ----- 1062  
240 uSerLeuValGluLysThrProAspGluAlaAlaProLeuValGluArgThrProAspTh 260  
1063 GGCTGAACTTGTGCGAAACACCTGACAGAGCTGCACGCTTGGTGGAGGAACTC 1122  
260 rAlaGluSerLeuValGluLysThrProAspGluAlaAlaSerLeuValGluGlyThrSe 280  
1123 TGCCTAAATCAATGTCTGGGAAAGCAACATCTCGAAAGTTTGAACAGTCAACAGAAGA 1182  
280 rAspLysIleGlnCysLeuGluLysAlaThrSerGlyLysPheGluGlnSerAlaGluG 300  
1183 ACACCTAGGAAATTTGGCGCTTACAAAGAAACATCTGAGAAATTTGATGCGCA-- 1240  
300 uThrProArgGluIleThrSerProAlaLysGluThrSerGluLysPheThrTrpProAl 320  
1240 ----- 1240  
320 aLysGlyArgProArgLysIleAlaTrpGluLysLysGluAspThrProArgGluIleMe 340  
1241 -----GCAAAAGAAAGATCTAGGAA 1260  
340 tSerProAlaLysGluThrSerGluLysPheThrTrpAlaLysGlyArgProArgLy 360  
1261 GATCATGCGGAGGAAAGAAACATCTCTAAGACTGAATCGCTGGCAGGAGTAACACC 1320  
360 sIleAlaTrpGluLysLysGluThrProValLysThrGlyCysValAlaArgValThrSe 380  
1321 TAATAAACTGAAGTTTGGAAAAAGCAACATCTAATATGATGTGATGCTCTCTACAAAAGA 1380  
380 rAsnLysThrLysValLeuGluLysGlyArgSerLysMetIleAlaCysProThrLysG 400  
1381 ACATCTCAAAAGCAAGTACAATGTGGATGTGAGTCTGTAGAGCCTATATTCAGTCT 1440  
400 uSerSerThrLysAlaSerAlaAsn----- 408  
1441 TTTTGGCACACGAGTATTGAAATTCACAGTGTACAAAAGTTGAGGAAGACTTTAATCT 1500  
408 ----- 408  
1501 TGCTACCAAGATTACTCTAAGAGTGTGCGACAGAAATTAACGTGTTACTGATGCTAC 1560  
408 ----- 408  
1561 ATATCAAAAGATATCAAAACAATAATCAAAATAGAGATCATGATGTTCCCATCAGA 1620  
409 -----AspGlnArgPheProSerG 415

1621 ATCCAAACGAGGAGAGATGAAGATATTTCTGGGATTTCTGGGAGTCTCTTTGAGAGTTC 1680  
415 uSerLysGlnGluAspGluGluTyrrSerCysAspSerArgSerLeuPheGluSerSe 435  
1681 TGCAAAAGACTCAAGTGTGTATACCTGAGTCTATGCTATCATCAAAAGTAAATGAGATAATAG 1740  
435 rAlaLysIleGlnValCysIleProGluSerIleTyrrGlnLysValMetGluLeuAsnAr 455  
1741 AGAAGTAGAGAGCTTCTGAGAGCCATCTGCTTCAAGCTTCCGCTGCGTNGCAATGCAAAA 1800  
455 gGluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGlnAs 475  
1801 GACTGTTTCCAAATAAGCCCTTGAATTTGAAGATGAACAAACATTGAGAGCAGCTCAGAT 1860  
475 nSerValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAspProme 495  
1861 GTTCCCATCAGATCCAAACAAAGGACGATGAAGAAATTTCTGGGATTTCTGAGAGTCC 1920  
495 tPheProGluSerLysGlnLysAspTyrrGluGluAsnSerTrpAspSerGluSerLe 515  
1921 CTGTGAGACGCTTTCACAGAGGATGTGATTTTACCCCAAGCTACACATCAAAAGAAAT 1980  
515 uCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluL 535  
1981 CGATACCTTAAGTGGAAATTTAGAAGAGTCTCTGTTTAAAGATGCTTCTGAAGCCTAC 2040  
535 eAspLysIleAsnGlyLysLeuGluGluSerProAsnLysAspGlyLeuLysAlaTh 555  
2041 CTGTGAGAGAAATTTCTTCCCAATTAAGCCTTAGAATTAAGGACAGAGAAACATT 2100  
555 rCysGlyMetLysValSerIleProThrLysAlaLeuGluLysAspMetGlnThrPh 575  
2101 CAAAGCAGAGTCTCTGAAAGATGCTCTCTGAAAGCTTACCTGTGGAAGGAAAGTTTC 2160  
575 eLysAlaGluProGlyLysProSerAlaPheGluPro----- 588  
2161 TCTTCCAAATAAGCCTTAGAATTAAGGACAGAGAAACATCAAGAGAGAGTCTCTGGA 2220  
589 -----AlaThrGluMetGlnLys----- 594  
2221 TAATGATGGTCTTCTCAAGCCTACCTGTGGAAGAAAGTTTCTTCCAAATAAGAGTTC 2280  
595 -----SerValProAsnLysAlaLe 601  
2281 AGAATTAAGGACAGAGAAACATTAAGAGAGCTCAGATGTTCCCATCAGATCCAAACA 2340  
601 uGluLysAsnGluGlnThrTrpArgAlaAspGluIleLeuProSerGluSerLysG 621  
2341 AAAGGATGATGAAGAAATTTCTGGGATTTTGAAGTTCCTTGTAGACTCTCTTACAGAA 2400  
621 nLysAspTyrrGluGluAsnSerTrpAspThrGluSerLeuCysGluThrValSerGlnLy 641  
2401 TGATGTGTGTTTACCAAGCTTACATCAAAAGAAATTCGATACCTTAAGTGGAAATTT 2460  
641 sAspValCysLeuProLysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLe 661  
2461 AGAAGAGTCTCTGATAAGATGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAGTCTCTCT 2520  
661 uGluGlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerI 681  
2521 TCCAAATAAGCCTTAGAATTTGAAGACAGAGAAACATTAAGAGAGAGATGTGAGTTC 2580  
681 eProThrLysAlaLeuLeuMetAspMetGlnThrPheLysAlaGluProProGluLy 701  
2581 TGTAGAGTCCATTCAGTCTTTTGGCAACCGACTACTGAAATTCACAGTCTACAAA 2640  
701 s----ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal-- 715  
2641 AGTTGAGGAAGACTTTAATCTTACTACCAAGGAGGAGCAACAAACAGTAACTGGACA 2700  
716 -----ProAsnLysAlaLeuGluLeuLy 723





Pred. No.: 2,38e-273 Length: 1341  
 Score: 3458.00 Matches: 740  
 Percent Similarity: 65.58% Conservative: 83  
 Best Local Similarity: 58.96% Mismatches: 159  
 Query Match: 53.63% Indels: 273  
 DB: 5 Gaps: 12

US-09-602-362E-26 (1-3673) x ABJ05537 (1-1341)

QY 349 ATGACAGTGGGAGGAGGCGTCAACCTGAACAAAGAGATATGAAGAGGAGGACTGCT 408  
 Db 1 MetThrLysArgLysLysThrIleAsnLeuAsnIleGlnAspAlaGlnLysArgThrAla 20  
 QY 409 CTACACTGGGCGTGTCTCAATGCCATGCAAGTAGTAACTTTCTGGTAGACAGAAAG 468  
 Db 21 LeuHisTrpAlaCysValAsnGlyHisGluGluValValThrPheLeuValAspArgLys 40  
 QY 469 TGCNGCTTAATGCTCTGATGCGGAGGAGGAGGACCTCTGATGAAGGCTCTCAATGC 528  
 Db 41 CysGlnLeuAspValLeuAspGlyGluHisArgThrProLeuMetLysAlaLeuGlnCys 60  
 QY 529 GAGAGGAGGAGCTTTGTSCAAATATCTCATAGATGCTGCTGATCTAAATATTATGTAGA 588  
 Db 61 HisGlnGluAla-CysAlaAsnIleLeuIleAspSerGlyAlaAspIleAsnLeuValAs 80  
 QY 589 TGTGTATGGCAACACGCTCTCCATTATGCGTTTATAGTGAGAAATTTATTAATGCTGC 648  
 Db 80 pValTyrGlyAsnMetAlaLeuHisTyrAlaValTyrSerGluIleLeuSerValVal 100  
 QY 649 AACACTGCTCTCTATGCTGAGTATCATCGAGTGCAAAACAGGCTAGCTCACACCCCT 708  
 Db 100 aLysLeuLeuSerHisGlyAlaValIleGluValHisAsnLysAlaSerLeuThrProLe 120  
 QY 709 TTTACTGGCCATACAGAAAGAGGAGCAACTGTGGAATTTTACTTAACAAATAATGC 768  
 Db 120 uLeuLeuSerIleThrLysArgSerGluGlnIleValGluPheLeuLeuIleLysAsnAl 140  
 QY 769 AAATGCAACGCAATTAATGAGTCTAAATGTCACAGCCCTCATGCTGCTATGGAAGG 828  
 Db 140 aAsnAlaAsnAlaValAsnLysTyrLysCysThrAlaLeuMetLeuAlaValCysHisGl 160  
 QY 829 CTCATCAGAGATAGTGGCATGCTTCTCAGCAAAATGTTGACGCTTTGTGTGAAGACAT 888  
 Db 160 ySerSerGluIleValGlyWetLeuLeuGlnGlnAsnValAspValPheAlaAlaAspIl 180  
 QY 889 ACATGCAATACCTGAGAGAGTATGCTCTGCTGCTGAGTAAATCATTCATCAACA 948  
 Db 180 eCysGlyValThrAlaGluHisTyrAlaValThrCysGlyPheHisHisIleHisGluGl 200  
 QY 949 ACTTTGGAAACATATACGAAATTTACTTAAATCCTCAAAATACCAATACCAAGGAAAC 1008  
 Db 200 nileMetGluTyrIleArgLysLeuSerLysAsnHisGlnAsnThrAsnProGluGlyTh 220  
 QY 1009 ATCTACGAAACACCTGATGAGCTGCACCTTGGGCTGCTGCTGCTGCTGCTGCTGCTG 1045  
 Db 220 rSerAlaGlyThrProAspGluAlaAlaProLeuAlaGluArgThrProAspThrAlaGl 240  
 QY 1046 -----GAAAGAACACCTGCAC 1062  
 Db 240 uSerLeuValGluLysThrProAspGluAlaAlaProLeuValGluArgThrProAspTh 260  
 QY 1063 GGCTGAAAGCTGCTGGAAGAAACACCTGACGAGCTGCACGCTTGGTGGAGGAGACGTC 1122  
 Db 260 rAlaGluSerLeuValGluLysThrProAspGluAlaAlaSerLeuValGluGlyThrSe 280  
 QY 1123 TGCCAAATTCATGCTGGGAAAGCAACATCTCGAAAGTTTGAACAGTCAACAGAGA 1182  
 Db 280 rAspLysIleGlnCysLeuGluLysAlaThrSerGlyLysPheGluGlnSerAlaGluGl 300  
 QY 1183 AACACCTAGGAAATTTGAGCGCTACAAAGAAACATCTGAGAAATTTTCATGCGCA-- 1240  
 Db 300 uThrProArgGluIleThrSerProAlaLysGluThrSerGluLysPheThrTrpProAl 320

QY 1240 ----- 1240  
 Db 320 aLysGlyArgProArgLysIleAlaTrpGluLysLysGluAspThrProArgGluIleMe 340  
 QY 1241 -----GCAAAAGAAAGATCTAGAA 1260  
 Db 340 tSerProAlaLysGluThrSerGluLysPheThrTrpAlaAlaLysGlyArgProArgLy 360  
 QY 1261 GATCACATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
 Db 360 sileAlaTrpGluLysLysGluThrProValLysThrGlyCysValAlaArgValThrSe 380  
 QY 1321 TATATAAATCGAGTTTGGAAAAAGGAAACATCTAATATGATTCATGCTTCCTACAAAAGA 1380  
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 QY 1381 AACATCTACAAAAGCAGTACAAATGCGATGTGAGTCTCTGTAGAGCTATATTCAGTCT 1440  
 Db 400 uSerSerThrLysAlaSerAlaAsn----- 408  
 QY 1441 TTTTGGCACACGGACTATTGAAAAATTCACAGTGTACAAAGTTGAGGAGACTTTTAATCT 1500  
 Db 408 ----- 408  
 QY 1501 TGTCTACCAAGATTCTCTAAGAGTGTGCGACAGAATTATACGTGTTTACCTGATGCTAC 1560  
 Db 408 ----- 408  
 QY 1561 ATATCAAAAAGATATCAAAAACAATAATCAAAAATAGAGATCAGATGTTCCCATCAGA 1620  
 Db 409 -----AspGlnArgPheProSerGl 415  
 QY 1621 ATCCAAACGAGAGAGATGAGAAATATTTCTGGGATTTCTGGAGTCTTTTGGAGGTTTC 1680  
 Db 415 uSerLysGlnGluGluAspGluLysSerCysAspSerArgSerLeuPheGluSerSe 435  
 QY 1681 TGCAAAAGACTCAAGTGTGTATCTGATGCTGATGATGATGATGATGATGATGATGATGATG 1740  
 Db 435 rAlaLysIleGlnValCysIleProGluSerIleTyrGlnLysValMetGluIleAsnAr 455  
 QY 1741 AGAAGTAGAAGAGCTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
 Db 455 gGluValGluGluProLysLysProSerAlaPheLysProAlaIleGluMetGlnAs 475  
 QY 1801 GACTGTTCCAAATCAAGGCTTTGAAATTGAAGATGAACAAACATTCAGAGCAGCTCAGAT 1860  
 Db 475 nSerValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAspProMe 495  
 QY 1861 GTTCCCATCAGAAATCCAAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920  
 Db 495 tPheProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSerLe 515  
 QY 1921 CTGTGAGAGGTTTTCAGAGAGGATGTTATTTACCCAAAGCTTACACATCAAAAGAAAT 1980  
 Db 515 uCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIl 535  
 QY 1981 CGATACCTTAAGTGGAAAATTAGAAGAGTCTCCTGTTAAAGATGGTCTTCTGAAGCTTAC 2040  
 Db 535 eAspLysIleAsnGlyLysLeuGluGluSerProAsnLysAspGlyLeuLeuLysAlaTh 555  
 QY 2041 CTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100  
 Db 555 rCysGlyMetLysValSerIleProThrLysAlaLeuGluLeuLysAspMeGlnThrPh 575  
 QY 2101 CAAAGCAGAGTCTCTCTGATAAAGATGCTTCTGAAAGCTTACCTGTGGAAGGAAAGTTTC 2160  
 Db 575 eLysAlaGluProProGlyLysProSerAlaPheGluPro----- 588  
 QY 2161 TCTTCCAAATAAGCCTTAGAATTAAGGACAGAGAAACACTCAAGAGAGAGTCTCCTGA 2220  
 Db 589 -----AlaThrGluMetGlnLys----- 594  
 QY 2221 TAATGATGGTCTTCTGAAAGCTTACCTGTGGAAGGAAAGTTTCTCTTCCAAATAAGCTTT 2280



Db 595 -----|||:|||||-----SerValProAsnLysAlaLe 601  
 QY 2281 AGAATTGAAGGACAGAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGAAATCAAAACA 2340  
 Db 601 uGluLeuLysAsnGluGlnThrTrpArgAlaAspGluLeuLeuProSerGluSerLysG 621  
 QY 2341 AAAGATGATGAAGAAATCTCTGGGATTTTCAGAGATTTCCCTGGAGATCTCTTACAGAA 2400  
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 QY 2401 TGATGTGCTTTACCCCAAGCTTACACATCAAAAGAAATTCGATACCTTAAGTGGAAATTT 2460  
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 QY 2461 AGAAGATCTCTCGTAAAGATGGTCTCTGAAGCTTACCTGTGAATCAAAATTTCTCT 2520  
 Db 661 uGluGlySerProValLysAspGlyLeuLeuLysAlaAsnGlyMetLysValSerIle 681  
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 Db 681 eProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLy 701  
 QY 2581 TGTAGAGTCCACATTCAGTCTTTTGGCAAAACCGACTACTGAAATTCACAGTCTACAAA 2640  
 Db 701 s-----ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal-- 715  
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 QY 2881 GACAACAATGGCAAAATAGAAGAGTCT----- 2908  
 Db 774 physIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCy 794  
 QY 2908 ----- 2908  
 Db 794 sArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLy 814  
 QY 2909 -----CCTGAAAGCCCTTCTCAGCTTTCAGCTGCGCACTGAAATGCAAACTCTGT 2958  
 Db 814 sAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerVa 834  
 QY 2959 TCCAAATAAGGCTTAGAATGAAGAATAAAACAAATTCAGAGCA----- 3004  
 Db 834 lProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPhePr 854  
 QY 3004 ----- 3004  
 Db 854 oSerGluSerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgG 874  
 QY 3004 ----- 3004  
 Db 874 uThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLy 894  
 QY 3005 -----GATTCAACTACCTATCAAAATCTTGGATGCATCTCCTTC 3045  
 Db 894 sIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSe 914  
 QY 3046 TTGTGAAGAGGAGGAAGTCTTAAAGAAAGATACCTGTGAACAAATTCAGACGAAATGGA 3105

Db 914 rCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetG 934  
 QY 3106 ACAAATGAAAAATAAGTTTGTCTACTACAAAAAGAACTCTCAGAACGCAAGAAATAAA 3165  
 Db 934 uGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLy 954  
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 QY 3226 TTTAAATCAAGAGAAAGAGAGAAATGTCGATATATTAAAGAAAAAATTAGACC 3285  
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 QY 3286 C-----GAAGAGCACTTAGCAAAAAAGCTTAGAAGTGAAGTGAACCAACTTGA 3330  
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 QY 3331 ACAGACTCTCAGATACAAGATATAGAAATGAAAGGTGAACAAGTAATTTGAATCAGGT 3390  
 Db 1014 uGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnVa 1034  
 QY 3391 TTCTCACACTCATGAAAGTGAATGATCTCTTTTCATGAAAAATTGCATGTTGAAAAAGGA 3450  
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 QY 3451 AATTGCCATGCTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3510  
 Db 1054 uIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTrpGlnGlnLysGluAs 1074  
 QY 3511 TAAATACCTTTGAGACATTAAGATTTTACAAGAAAAAGATGCTCAACTTCAAAATGACCCCT 3570  
 Db 1074 nLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLe 1094  
 QY 3571 AAACTGAAACAGAAACACATACAAAAGGGCATCTCAGTATAGAGACGAGCTTAAAGT 3630  
 Db 1094 uLysLeuLysGluGlnLysLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysVa 1114  
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 ABJ37784  
 ID ABJ37784 standard; protein; 1341 AA.  
 XX  
 AC ABJ37784;  
 DX  
 DT 15-MAY-2003 (first entry)  
 DE Human tumour-related protein - SEQ ID No 565.  
 DE Human; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 KW tumour; breast cancer; cancer; immune response stimulation.  
 KW Homo sapiens.  
 OS  
 XX WO200283956-A1.  
 XX  
 XX 24-OCT-2002.  
 XX  
 XX 15-APR-2002; 2002WO-US012378.  
 XX  
 XX 13-APR-2001; 2001US-00834759.  
 PR 07-DEC-2001; 2001US-00007805.  
 PR 13-FEB-2002; 2002US-00076622.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;  
 PI Vedvick TS, McNeill PD, Durham M;  
 XX

DR WPI; 2003-103376/09.  
XX New polypeptide and polynucleotide useful for stimulating and/or  
PT expanding T cells specific for a tumor protein and treating breast  
PT cancer.  
XX  
PS Example 9; Page 342-346; 375pp; English.  
XX  
CC The invention comprises a method of stimulating and/or expanding T cells  
CC specific for a tumor protein. The invention further comprises human  
CC nucleic acids and proteins that are associated with tumors (e.g. breast  
CC cancer). The method and sequences of the invention are useful for  
CC stimulating and/or expanding T cells specific for a tumor protein,  
CC detecting the presence of cancer, stimulating an immune response in a  
CC patient and treating breast cancer. The present amino acid sequence  
CC represents a human tumor-related protein  
XX  
SQ Sequence 1341 AA;  
  
Alignment Scores:  
Pred. No.: 2,38e-273 Length: 1341  
Score: 3458.00 Matches: 740  
Percent Similarity: 65.58% Conservative: 83  
Best Local Similarity: 58.96% Mismatches: 159  
Query Match: 53.63% Indels: 273  
DB: 6 Gaps: 12  
  
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QY 349 ATCACAGTGGGAAAGAGCCCTCAACCTGAAACAAAGAGATATGAAGAGAGGACTGCT 408  
DB 1 MetThrLysArgLysLysThrIleAsnLeuAsnIleGlnAspAlaGlnLysArgThrAla 20  
QY 409 CTACATGGCCCTGCTCAATGCCATGCCATGCAAGTAGTAACTTTCTGGTAGACAGAAG 468  
DB 21 LeuHisTrpAlaCysValAsnGlyHisGluGluValValThrPheLeuValAspArgLys 40  
QY 469 TGCNCGCTTAATGCTCTGATGCGAAGGAGGACACCTCTCATGAAGCTCTCAACATGC 528  
DB 41 CysGlnLeuAspValLeuAspGlyGluHisArgThrProLeuMetLysAlaLeuGlnCys 60  
QY 529 GAGAGGAAGCTTTGTGCAAAATATCTCATAGATGCTGTGCTGATCTAAATATGTAGA 588  
DB 61 HisGlnGluAla-CysAlaAsnIleLeuIleAspSerGlyAlaAspIleAsnLeuValAs 80  
QY 589 TGTGTATGCAACACGGCTCTCATATGCTGCTTATAGTGAGAAATTTATTAATGCTGCG 648  
DB 80 pValTyrGlyAsnMetAlaLeuHisTyrAlaValTyrSerGluIleLeuSerValValAl 100  
QY 649 AACACTGCTGCTCTATGCTGAGTATCGAGGTGCAAAACAGGCTAGCCTCACACCCCT 708  
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QY 709 TTTACTGGCCATCAGAAAGAGCAAGCAAACTGTGGATTTTACTAACCAAAAATGC 768  
DB 120 uLeuLeuSerIleThrLysArgSerGlnIleValGluPheLeuLeuIleLysAsnAl 140  
QY 769 AAATGCAACGCAATTTAATGAGTCTAAATGCAAGCCCTCATGCTTGGCATATGTGAAGG 828  
DB 140 AsnAlaAsnAlaValAsnLysTyrLysCysThrAlaLeuMetLeuAlaValCysHisGl 160  
QY 829 CTCATCAGAGATAGTGGCATGCTTCTTTCAGCAAAATGTGACGTCTTTGCTGAAGACAT 888  
DB 160 ySerSerGluIleValGlyMetLeuLeuGlnGlnAsnValAspValPheAlaAlaAspIl 180  
QY 889 ACATGGAATAACTGCAGACAGTATGCTGCTGCTGCTGAGTAAATTCATTCATCAACA 948  
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QY 949 ACTTTTGGACATATACGAAATATCTCAAAATCTCAAAATACCAATCCAGAGAGAAC 1008  
DB 200 nIleMetGluTyrIleArgLysLeuSerLysAsnHisGlnAsnThrAsnProGluGlyTh 220

QY 1009 ATCTACAGGAACACCTGATGAGGCTGCACCCCTTGGCG- 1045  
DB rSerAlaGlyThrProAspGluAlaAlaProLeuAlaGluArgThrProAspThrAlaGl 240  
QY 1046 -----GAAAGAACACCTGCAC 1062  
DB 240 uSerLeuValGluLysThrProAspGluAlaAlaProLeuValGluArgThrProAspTh 260  
QY 1063 GGCTGAAAGCTTCTGCAAAAAACACCTGACAGGCTGCACGCTTGGTGAGGAACGTC 1122  
DB rAlaGluSerLeuValGluLysThrProAspGluAlaAlaSerLeuValGluGlyThrSe 280  
QY 1123 TGCACAAATTCATGCTGGGAAAGCAACATCTGAAAGTTTGAACAGTCAACACAGA 1182  
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QY 1183 AACACCTTAGGAAATTTGAGGCTTACAAAGAAACATCTGAGAAATTTTCATGGCCA- 1240  
DB 300 uThrProArgGluIleThrSerProAlaLysGluThrSerGluLysPheThrTrpProAl 320  
QY 1240 ----- 1240  
DB 320 aLysGlyArgProArgLysIleAlaTrpGluLysLysGluAspThrProArgGluIleMe 340  
QY 1241 -----GCAAAAGAAAGATCTAGGAA 1260  
DB tSerProAlaLysGluThrSerGluLysPheThrTrpAlaAlaLysGlyArgProArgL 360  
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QY 1381 AACATCTACAAAAAGCAAGTACAAATGTGGATGTGAGTTCTGTAGACCTATATTCAGTCT 1440  
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QY 1441 TTTTGGCACACGGACTATTGAAAATTCACAGTGTACAAAAGTTGAGGAAGACTTTAATCT 1500  
DB 408 ----- 408  
QY 1501 TGTACCAAGATATTCTTAAGAGTGTGCACAGAATTTATACGTGTTTACCTGATGCTAC 1560  
DB 408 ----- 408  
QY 1561 ATATCAAAAAGATATCAAAAATAATCAAAAATAGAGATCAGATGTTCCCATCAGA 1620  
DB 409 -----AspGlnArgPheProSerGl 415  
QY 1621 ATCCAAACGAGAGCAGATCAAGATATTCTTGGGATCTCTGGGAGTCTCTTTGAGAGTTC 1680  
DB 415 uSerLysGlnGluAspGluGluTyrSerCysAspSerArgSerLeuPheGluSerSe 435  
QY 1681 TGCACAGCTCAAGTGTGTATACCTGAGTCTATGTATCAGAAAGTAAATGGAGATAATAG 1740  
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QY 1741 AGAAGTAGAAGAGCTTCTGAGAGCCATCTGCTTCAAGCCCTGCGCTGAAATGCAAAA 1800  
DB 455 gGluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGlnAs 475  
QY 1801 GACTGTTTCCAAATAAGCCTTTCAATGAAGATGAACAAACATTCAGAGAGCTCAGAT 1860  
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QY 1861 GTTCCCATCAGAAATCCAAACAAAGAGCAGATGAAGAAAATCTTGGGATTTCTGAGAGTCC 1920  
DB 495 tPheProProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSerLe 515  
QY 1921 CTGTGACAGCGTTTTCAGAGAGGATGTGATTATTTACCCCAAGCTTACACATCAAAAAGAAAT 1980

515 uCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluI 535  
1981 CGATACCTTAAGTGGAAATTAAGAGAGCTCTCTGTTAAAGATGGTCTTCTGAAGCCTAC 2040  
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2041 CTGTGGAAGAAAGTTTCTTCCAAATAAAGCCTTAGAATTAAGAGGACAGAGAACATTT 2100  
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2101 CAAAGCAGAGTCTCTGTAATAAGATGGTCTTCTGAAGCCTACCTGTGGAGGAAAGTTTC 2160  
575 eLysAlaGluProProGlyLysProSerAlaPheGluPro----- 588  
2161 TCTTCCAAATAAGCCTTAGAATTAAGGACAGAGAAACACTCAAAGCAGAGTCTCCTGA 2220  
589 -----AlaThrGluMetGlnLys----- 594  
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595 -----SerValProAsnLysAlaLe 601  
2281 AGAATTGAAGGACAGAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGAAATCCAAACA 2340  
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2401 TGATGTGTTTACCCAGGCTACACATCAAAGAAATTCGATACCTTAAGTGGAAATTT 2460  
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661 uGluGlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerI 681  
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701 s----ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal-- 715  
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716 -----ProAsnLysAlaLeuGluLeuL 723  
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754 sGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAs 774  
2881 GACACAAATGCAAAATAGAGACTCT----- 2908  
774 pLysIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCy 794  
2908 ----- 2908  
794 sArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheL 814  
2909 -----CCTGAAAGCCTTCTCACTTTGAGCGCTGCCACTGAAATGCAAAACTCTGT 2958  
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3004 ----- 3004  
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3004 ----- 3004  
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3005 -----GATTCAACTTACCTTCAAAATCTTGGATGCACCTTCCTC 3045  
894 sIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHis 914  
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RESULT 7  
ABR47548  
ID ABR47548 standard; protein; 1341 AA.  
XX  
AC ABR47548;  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Breast cancer associated protein sequence SEQ ID NO:334.  
XX  
KW Human; breast cancer; cytostatic; gene therapy.

XX OS Homo sapiens.  
 XX PN WO2003004989-A2.  
 XX PD 16-JAN-2003.  
 XX PF 21-JUN-2002; 2002WO-US019669.  
 XX PR 21-JUN-2001; 2001US-0299887P.  
 XX PR 27-JUN-2001; 2001US-0301572P.  
 XX PR 18-JUL-2001; 2001US-0306501P.  
 XX PR 25-SEP-2001; 2001US-0325002P.  
 XX PR 03-MAR-2002; 2002US-0362585P.  
 XX PR 14-MAY-2002; 2002US-0380391P.  
 XX (MILL-) MILLENIUM PHARM INC.  
 XX PA Lillie J, Gannavarapu M, Glatt K, Hoerish S, Kamatkar S;  
 XX PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
 XX PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;  
 XX DR WPI; 2003-210381/20.  
 XX DR N-PSDB; ACC50246.  
 XX PT Breast cancer diagnosis or treatment by comparing the level of expression  
 XX PT of a marker in a patient sample with that in the control non-breast  
 XX PT cancer sample.  
 XX PS Claim 1; SEQ ID NO 334; 128pp; English.  
 XX CC The present invention describes a method for assessing whether a patient  
 XX CC is afflicted with breast cancer. The method comprises comparing the level  
 XX CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
 XX CC ABR47386 to ABR47632) in a patient sample and the normal level of  
 XX CC expression of the marker in a control non-breast cancer sample, where a  
 XX CC significant increase in the level of expression of the marker in the  
 XX CC patient sample and the normal level is an indication that the patient is  
 XX CC afflicted with breast cancer. The breast cancer associated sequences from  
 XX CC the present invention have cytostatic activities and can be used in gene  
 XX CC therapy. The method is useful for diagnosing and treating breast cancer.  
 XX CC N.B. The sequence data for this patent did not form part of the printed  
 XX CC specification, but was obtained in electronic format directly from WIPO  
 XX CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 1341 AA;  
 Alignment Scores:  
 Pred. No.: 2,38e-273 Length: 1341  
 Score: 3458.00 Matches: 740  
 Percent Similarity: 65.58% Conservative: 83  
 Best Local Similarity: 58.96% Mismatches: 159  
 Query Match: 53.63% Indels: 273  
 DB: 6 Gaps: 12  
 US-09-602-362E-26 (1-3673) x ABR47548 (1-1341)  
 QY 349 ATGACAGTAGGGAAGAGCCGCTCAACCTGAACAAAGAGATATGAGGAAGAGGACTGCT 408  
 Db 1 MetThrLysArgLysLysThrIleAsnLeuAsnIleGlnAspAlaGlnLysArgThrAla 20  
 QY 409 CTACACTGGCCGTGTGTCATGCGCCATGCANAGTAGTAACATTTCTGCTAGACAGAAAG 468  
 Db 21 LeuHisTrpAlaCysValaAsnGlyHisGluGluValValThrPheLeuValAspArgLys 40  
 QY 469 TGCNGCTTAATGCTCTGTATGCGGAGGAGGACACCTCTGATGAAGGCTCTCAATGCG 528  
 Db 41 CysGlnLeuAspValLeuAspGlyGluHisArgThrProLeuMetLysAlaLeuGlnCys 60  
 QY 529 GAGAGGGAAGCTTTGTGCAATATTTCTCATAGATGCTGGTGTGATCTAAATTAATGTAGA 588  
 Db 61 HisGlnGluAla-CysAlaAsnIleLeuIleAspSerGlyAlaAspIleAsnLeuValAs 80

QY 589 TGTGTATGGCAACACAGGCTCTCCATTATGCGCTTTATAGTGAGAAATTTATTATGTGGC 648  
 Db 80 pValTyrGlyAsnMetAlaLeuHisTyrAlaValTyrSerGluIleLeuSerValValAl 100  
 QY 649 AACACTGCTCTCTATGTCAGTCTCATCGAGGTGCAAAACAGGCTAGCTCACCCCT 708  
 Db 100 aLysLeuLeuSerHisGlyAlaValIleGluValHisAsnLysAlaSerLeuThrProLe 120  
 QY 709 TTTACTGGCCATACAGAAAGCAAGCAAACTGTGGAATTTTACTACAAAAATGC 768  
 Db 120 uLeuLeuSerIleThrLysArgSerGluGlnIleValGluPheLeuLeuIleLysAsnAl 140  
 QY 769 AAATGCAACGCAATTTAATGAGTCTAAATGACAGCCCTCATCTGCGCATATGTGAAG 828  
 Db 140 aAsnAlaAsnAlaValAsnLysTyrLysCysThrAlaLeuMetLeuAlaValCysHisG 160  
 QY 829 CTCTACAGATAGTCGGCATGCTTCTTCAGCAAAATGTTGAGCTCTTTGCTGAACACAT 888  
 Db 160 ySerSerGluIleValGlyMetLeuLeuGlnAsnValAspValPheAlaAlaAspAl 180  
 QY 889 ACATGGAATAACTGCAGAACGTTTATGCTGCTGCTGCTGGAGTTAATTACATTCATCAAC 948  
 Db 180 eCysGlyValThrAlaGluHisTyrAlaValThrCysGlyPheHisIleHisGluGl 200  
 QY 949 ACTTTTGGACATATACGAAATTTACTTAAATCTCAAAATACCAATCCAGATCCAGAAAGAC 1008  
 Db 200 nIleMetGluTyrIleArgLysLeuSerLysAsnHisGlnAsnThrAsnProGluGlyTh 220  
 QY 1009 ATCTACAGGAACACCTGATGAGGTGCACCTTTGGGG- 1045  
 Db 220 rSerAlaGlyThrProAspGluAlaAlaProLeuAlaGluArgThrProAspThrAlaGl 240  
 QY 1046 -----GAAAGAACCTCACAC 1062  
 Db 240 uSerLeuValGluLysThrProAspGluAlaAlaProLeuValGluArgThrProAspTh 260  
 QY 1063 GGCTGAAGCTTGTGGAAAAACACCTGACGAGGTGCACGCTTGGTGAGGGAACGCTC 1122  
 Db 260 rAlaGluSerLeuValGluLysThrProAspGluAlaAlaSerLeuValGluGlyThrSe 280  
 QY 1123 TGCACAAATTCATGCTCGGGAAAGCAACATCTGGAAGCTTTGAACAGTCAACAGAGA 1182  
 Db 280 rAspLysIleGlnCysLeuGluLysAlaThrSerGlyLysPheGluGlnSerAlaGluGl 300  
 QY 1183 AACACCTAGGAAATTTTGAGGCTACAAAGAAACATCTGAGAAATTTTCATGGCCA- 1240  
 Db 300 uThrProArgGluIleThrSerProAlaLysGluThrSerGluLysPheThrTrpProAl 320  
 QY 1240 ----- 1240  
 Db 320 aLysGlyArgProArgLysIleAlaTrpGluLysLysGluAspThrProArgGluIleMe 340  
 QY 1241 -----GCAAGAAAGATCTAGAA 1260  
 Db 340 tSerProAlaLysGluThrSerGluLysPheThrTrpAlaAlaLysGlyArgProArgLy 360  
 QY 1261 GATCACATGGGAGAAAAAGAAACATCTGTAAGACTGAATGCTGGCAGGAGTAACACC 1320  
 Db 360 sIleAlaTrpGluLysLysGluThrProValLysThrGlyCysValAlaArgValThrSe 380  
 QY 1321 TAATAAACCTGAAGTTTTGGAAAAAGGAACATCTAATATGATTCATGCTCTCACAAGA 1380  
 Db 380 rAsnLysThrLysValLeuGluLysGlyArgSerLysMetIleAlaCysProThrLysGl 400  
 QY 1381 AACATCTACAAAACCAAGTACAAATGGATGTGAGTCTCTGTAGAGCTATATTCTAGTCT 1440  
 Db 400 uSerSerThrLysAlaSerAlaAsn----- 408  
 QY 1441 TTTTGGCACACGGACTATTGAAAATTCACAGTGTACAAAAGTTGAGGAAGACTTTTAACT 1500  
 Db 408 ----- 408  
 QY 1501 TGCTACCAAGATTATCTTAAGAGTGTGCACAGAAATTTACGNGTTTACCTGTATGCTAC 1560

Db 408 ----- 408  
QY 1561 ATATCAAAAGATATCAAAACRAATAAATCACAAATAGAGATCAGATGTTCCCATCAGA 1620  
Db 409 ----- 409  
QY 1621 ATCCAAACGAGAGAGATGAAGAATATTCTTGGGATTTCTGGAGTCTCTTTGAGAGTTC 1680  
Db 415 uSerLysGlnGluProLysAspGluTyrSerCysAspSerArgSerLeuPheGluSerSe 435  
QY 1681 TGCAAAAGACTCAAGTGTGTATACCTCAGTCTATGATCAGAAAGTAATCGAGATAAATAG 1740  
Db 435 rAlaLysIleGlnValCysIleProGluSerIleTyrGlnLysValMetGluLileAsnAr 455  
QY 1741 AGAAGTAGAAGACTCTTCGAGAGCCATCTGCTTCAAGCTGCGGNGAAATCAAAA 1800  
Db 455 gGluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGlnAs 475  
QY 1801 GACTGTTCCAAATAAAGCTTTGAATTGAAGTAATGAACAAACATTTGAGAGAGCTCAGAT 1860  
Db 475 nSerValProAsnLysAlaPheGluLysAsnGluGlnThrLeuArgAlaAspProWe 495  
QY 1861 GTTCCCATCAGATCCAAACAAAGAGCAGATGAAGAAATTTCTGGGATTTCTGAGAGTCC 1920  
Db 495 tPheProProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSerLe 515  
QY 1921 CNGTGAGACGGTTTCACAGAGGATGTGTATTACCCAAAGCTACACATCAAAAGAAATT 1980  
Db 515 uCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIl 535  
QY 1981 CGATACCTTTAAGTGGAAATTAAGAAGTCTCCTGTTAAAGATGCTCTTCTGAAGCTTAC 2040  
Db 535 eAspLysIleAsnGlyLysLeuGluGluSerProAsnLysAspGlyLeuLeuLysAlaTh 555  
QY 2041 CTGTCGAAGAAAGTTTCTCTCCAAATTAAGCCTTAGAATTAAGGACAGAGAAACATT 2100  
Db 555 rCysGlyMetLysValSerIleProThrLysAlaLeuGluLysAspMetGlnThrPh 575  
QY 2101 CAAAGCAGAGTCTCCTGTATAAGTGTCTTCTGAAGCTACCTGTGGAAGGAAGTTTC 2160  
Db 575 elysAlaGluProProGlyLysProSerAlaPheGluPro----- 588  
QY 2161 TCTTCCAAATAAGCCTTAGAATTAAGGACAGAGAAACACTCAAGACAGAGTCTCCTGA 2220  
Db 589 -----AlaThrGluMetGlnLys----- 594  
QY 2221 TAATGATGCTCTCTGAAGCTTACCTGTGGAGGAAGATTCTCTTCCAAATAAGCTTT 2280  
Db 595 -----SerValProAsnLysAlaLe----- 601  
QY 2281 AGAATTGAAGGACAGAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGAAATCCAAACA 2340  
Db 601 uGluLeuLysAsnGluGlnThrTrpArgAlaAspGluIleLeuProSerGluSerLysGl 621  
QY 2341 AAAGCATGATGAGAAATTTCTGGATTTTGAGAGTTTCTCTGAGACTCTCTTACAGAA 2400  
Db 621 nLysAspTyrGluGluAsnSerTrpAspThrGluSerLeuCysGluThrValSerGlnLy 641  
QY 2401 TGATGTGTGTTTACCACAGGCTACACATCAAAAAGAAATTCGATACCTTTAAGTGAATAAT 2460  
Db 641 sAspValCysLeuProLysAlaAlaHisGlnLysGluLileAsnGlyLysLe 661  
QY 2461 AGAAGAGTCTCTGTATAAGATGTCTTCTGAAGCTTACCTGTGGAATGAATAATTTCTCT 2520  
Db 661 uGluGlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIl 681  
QY 2521 TCCAAATAAGCCTTAGAATTAAGGACAGAGAAACATTCAAAGCAGAGGATGTGAGTTC 2580  
Db 681 eProThrLysAlaLeuGluLeuMetAspWeGlnThrPheLysAlaGluProProGluLy 701  
QY 2581 TGTAGAGTCCACATTCACTCTTTTGGCAAAACCGACTACTGAAAATTACAGTCTACAAA 2640  
Db ----- 2640

Db 701 s---ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal-- 715  
QY 2641 AGTTGAGGAAGACTTTAATCTTACTACCAAGGAGGAGCAACAAGACAGTAACCTGGACA 2700  
Db 716 -----ProAsnLysAlaLeuGluLeuLy 723  
QY 2701 ACAGAAAGCTGATATTGGCATATTATGAACGAGCTCCACAAGATCAAAACAAATAAGATGCC 2760  
Db 723 sAsnGluGlnThrLeuArgAlaAspGluIleLeuPro----- 735  
QY 2761 CACATCAGAATTAGGAAGAAAGAGATACAAATCAACTTCAGATTCTCAGATTATATCTC 2820  
Db 736 -----SerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCy 754  
QY 2821 TGTGAGTGATACACAGAAATTATGAGTGTCTTACCTGAGGCTACATATCAAAAGAAATAAAA 2880  
Db 754 sGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLileAs 774  
QY 2881 GACAACAATGGCAAAATAGAGAGTCT----- 2908  
Db 774 pLysIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCy 794  
QY 2908 ----- 2908  
Db 794 sArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLy 814  
QY 2909 -----CCTGAAAGGCTTCTCACTTTGAGCCTGCCACTGAAATTCGAAAACCTCTGT 2958  
Db 814 sAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerVa 834  
QY 2959 TCCAAAATAAGGCTTAGAATGGAAGATAAACAACAACTTCAGAGCA----- 3004  
Db 834 lProAsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPhePr 854  
QY 3004 ----- 3004  
Db 854 oSerGluSerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGl 874  
QY 3004 ----- 3004  
Db 874 uThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLy 894  
QY 3005 -----GATTCAACTACCTTATCAAAAATCTTGATGATCACTCTCTTC 3045  
Db 894 sIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSe 914  
QY 3046 TTCTGAAAGAGGAGGAACTTAAAGATAACTGTGACAAATTTACAGCAAAATGGA 3105  
Db 914 rCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGl 934  
QY 3106 ACAAATCAAAAATAAGTTTGTCTACTACAAAAGGAACTGTGACAGCGAAAGAAATAAA 3165  
Db 934 uGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLileLy 954  
QY 3166 ATCAGAGTTAGAGAACCAAAAGCTAAATGGGAAACAGAGCTCTGCAGTGTGAGATTGCC 3225  
Db 954 sSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuth 974  
QY 3226 TTTAAATCAAGAGAGAGAGAGAGAAATGTCGATATATTAAAGAAAAAATTAGACC 3285  
Db 974 rLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGl 994  
QY 3286 C-----GAAGACCACTTAGGAAAAGTTAGAGTGAACACCAACTTGA 3330  
Db 994 uGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGl 1014  
QY 3331 ACAGACTCTCAGAAATACAGATATAGAAATTAAGAGTGTAAACAGTAATTTGAATCAGGT 3390  
Db 1014 uGlnAlaLeuArgIleGlnAspIleGluAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnVa 1034  
QY 3391 TTCTCACTCATGAAAGTGAATAATGATCTCTTTTATGAAAATTGATCTTCTGAAAAGGA 3450  
Db 1034 lSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGl 1054

QY 3451 RATTGCGCATGTAAACTGGAGTAGCCACACTGAAACATCAACACAGGTGAAGGAAA 3510  
 Db 1054 uilealaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnIleValGlnGluLysGluAs 1074  
 QY 3511 TAAATPACTTTGAGGACATTAAAGATTTTACAGAAAAGAAATGCTCAACTTCAAAATGACCCCT 3570  
 Db 1074 nlystYrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLe 1094  
 QY 3571 AAARCTGAAACAGAAACAGTAACAAAAGGCACTCTCAGTATAGAGAGAGAGAGTAAAGT 3630  
 Db 1094 uLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnIleValGlnMetLysVa 1114  
 QY 3631 TGTGAGGCGCAGAGAACAGTGTGCTGCTTCTTAAATTCAGAGAA 3673  
 Db 1114 lleuileAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 1128

## RESULT 8

ABJ37788  
 ID ABJ37788 standard; protein; 1349 AA.

XX ABJ37788;

XX 15-MAY-2003 (first entry)

XX Human tumour-related protein - SEQ ID No 573.

XX Human; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 tumour; breast cancer; cancer; immune response stimulation.

XX Homo sapiens.

XX WO200283956-A1.

XX 24-OCT-2002.

XX 15-APR-2002; 2002WO-US012378.

XX 13-APR-2001; 2001US-00834759.

XX 07-DEC-2001; 2001US-00007805.

XX 13-FEB-2002; 2002US-00076622.

XX (CORI-) CORIXA CORP.

XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 Mitcham JL, Xu J, Hazlock SL, Hepler WT, Henderson RA, Fanger CR;  
 Vedvick TS, McNeill PD, Durham M;

XX WPI; 2003-103376/09.

XX New polypeptide and polynucleotide useful for stimulating and/or  
 expanding T cells specific for a tumor protein and treating breast  
 cancer.

XX Example 12; Page 353-357; 375pp; English.

XX The invention comprises a method of stimulating and/or expanding T cells  
 specific for a tumour protein. The invention further comprises human  
 nucleic acids and proteins that are associated with tumours (e.g. breast  
 cancer). The method and sequences of the invention are useful for  
 stimulating and/or expanding T cells specific for a tumour protein,  
 detecting the presence of cancer, stimulating an immune response in a  
 patient and treating breast cancer. The present amino acid sequence  
 represents a human tumour-related protein

XX Sequence 1349 AA;

## Alignment Scores:

Pred. No.: 7,07e-272 Length: 1349  
 Score: 3440.00 Matches: 737  
 Percent Similarity: 65.39% Conservative: 83  
 Best Local Similarity: 58.77% Mismatches: 161  
 Query Match: 53.35% Indels: 273

DB: 6 Gaps: 12  
 US-09-602-362E-26 (1-3673) x ABJ37788 (1-1349)  
 QY 352 ACAGTAGGAGAGAGCCCGTCACACCTGCAACAAAGAGATATGAAGAAGAGGAGCTGCTCTA 411  
 Db 10 ThrLysArgLysLysThrIleAsnLeuAsnIleGlnAspAlaGlnLysArgThrAlaLeu 29  
 QY 412 CACTGGCCCTGTCTCAATGCGCCATGCANAAAGTAGTACATTTCTGTAGACAGAAAGTGC 471  
 Db 30 HistpAlaCysValAsnGlyHisGluGluValValThrPheLeuValAspArgLysCys 49  
 QY 472 CNGCTTAATCTCCCTTGCAGGAGGAGGAGACACCTCTCATCAAGGCTCTTCAATGCGCAG 531  
 Db 50 GlnProAspValLeuAspGlyGluHisArgThrProLeuMetLysAlaLeuGlnCysHis 69  
 QY 532 AGGAAGCTTTGCAAAATATCTCATAGATGCTGTGCTGCTCTAAATATGATGAGTGT 591  
 Db 70 GlnGluAla-CysAlaAsnIleLeuIleAspSerGlyAlaAspIleAsnLeuValAspVa 89  
 QY 592 GTATGGCAACACGCGCTCTCCATTATGCGCTTTTATAGTGAATTTTAAATGCTGCGCAAC 651  
 Db 89 lTyrGlyAsnMetAlaLeuHisTyrAlaValTyrSerGluIleLeuSerValValAlaLys 109  
 QY 652 ACTGCTGTCTTATGCTGAGTCTCATGAGTGCAGGTCGCAAAAGGCTGCTCACACCCCTTT 711  
 Db 109 sLeuLeuSerHisGlyAlaValIleGluValHisAsnLysAlaSerLeuThrProLeuLe 129  
 QY 712 ACTGGCCATACAGAAAAGCAAGCAAACTCTGGAAATTTTACTTAACAAAAATGCAAA 771  
 Db 129 uLeuSerIleThrLysArgSerGluGlnIleValGluPheLeuLeuIleLysAsnAlaAs 149  
 QY 772 TGCAAAGCGATTTAATGAGTCTAAATGACAGCCCTCATGCTGCGCATATGTGAAGGCTC 831  
 Db 149 nAlaAsnAlaValAsnLysLysCysThrAlaLeuMetLeuAlaValCysHisGlyLe 169  
 QY 832 ATCAGAGATAGTCGGCATGCTTCTTACGAAATGTTGACGCTCTTTGTCGAGACATACA 891  
 Db 169 uSerGluIleValGlyMetLeuLeuGlnGlnAsnValAspValPheAlaAlaAspIleCy 189  
 QY 892 TGAATAACTGCGAGACGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951  
 Db 189 sGlyValThrAlaGluHisTyrAlaValThrCysGlyPheHisHisIleHisGluGlnIle 209  
 QY 952 TTGGAACATATACGAAAAATACCTAAATAATCCTCAAAATACCAATCCAGAGGAAACATC 1011  
 Db 209 eMetGluTyrIleArgLysLeuSerLysAsnHisGlnAsnThrAsnProGluGlyThrSe 229  
 QY 1012 TACAGGAACACCTGATGAGGCTGCGACCCCTTGGCG----- 1045  
 Db 229 rAlaGlyThrProAspGluAlaAlaProLeuAlaGluArgThrProAspThrAlaGluSe 249  
 QY 1046 -----GAAAGAACACCTGACAGCGC 1065  
 Db 249 rLeuValGluLysThrProAspGluAlaAlaProLeuValGluArgThrProAspThrAl 269  
 QY 1066 TGAAGCTTGTGGAAAAACACCTGACAGGCTGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125  
 Db 269 aGluSerLeuValGluLysThrProAspGluAlaAlaSerLeuValGluGlyThrSerAs 289  
 QY 1126 CAAATTCATCTCTGGGAAAGCAACATCTGGAAAGTTTGAACAGTCAACAGAGAAAC 1185  
 Db 289 pLysIleGlnCysLeuGluLysAlaThrSerGlyLysPheGluGlnSerAlaGluGluTh 309  
 QY 1186 ACTAGCAAAATTTGAGCCCTTACAAAAGAACATCTGAGAAATTTTCATGCCCA----- 1240  
 Db 309 rProArgGluIleThrSerProAlaLysGluThrSerGluLysPheThrTrpProAlaLys 329  
 QY 1240 ----- 1240  
 Db 329 sGlyArgProArgLysIleAlaTrpGluLysLysGluAspThrProArgGluIleMetSe 349  
 QY 1241 -----GCAAAAGAAAGATCTAGGAAGAT 1263

Db 349 rProAlaLysGluThrSerGluLysPheThrTrpAlaAlaLysGlyArgProArgLysI 369  
QY 1264 CACATGGAGGAAAAAGAACATCTGTAAAGACTGAATCGCGGAGGAGTAACCTAA 1323  
Db 369 eAlaTrpGluLysLysGluThrProValLysThrGlyCysValAlaArgValThrSerAs 389  
QY 1324 TAAACTGAAGTTTTCGAAAAAGAACATCTAATATGATTGATGCTCTACAAAAGAAC 1383  
Db 389 nLysThrLysValLysGluLysGlyArgSerLysMetIleAlaCysProThrLysGluSe 409  
QY 1384 ATCTACAAAAGCAAGTACAAATGTGATGTGAGTCTGTAGAGCCTATATTCAGTCTTT 1443  
Db 409 rSerThrLysAlaSerAlaAsn 416  
QY 1444 TGGCACACGGACTATTGAAAATTCACAGTGTACAAAAGTTGAGGAAGACTTTAATCTTGC 1503  
Db 416 416  
QY 1504 TACCAAGATTATCTCTAAGAGTCTGCACAGAAATTATACGTGTTTACCTGATGCTACATA 1563  
Db 416 416  
QY 1564 TCAAAAAGATATCAAAAACAATAATCACAAAATAGAGATCAGATGTTCCCATCAGAAATC 1623  
Db 417 417  
QY 1624 CAAACGAGAGAGATGAAGATATATCTTGGGATTCGGGATCTCTTTGAGAGTTCTGC 1683  
Db 424 rLysGluGluLysGluLysSerCysAspSerArgSerLeuPheGluSerSerAl 444  
QY 1684 AAAGACTCAAGTGTGTATACCTGAGTCTATGATGATCAGAAAGTAATGGAGATAATAGAGA 1743  
Db 444 aLysIleGlnValCysIleProGluSerIleThrGlnLysValMetGluIleAsnArgG 464  
QY 1744 AGTAGAGAGCTCTCTGAGAACCCATCTGCTTCAAGCTCGCGTNGAAATGCAAAAGAC 1803  
Db 464 vAlGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGlnAsnSe 484  
QY 1804 TGTTCCAAATAGCTTTGAATTAAGATGAAGATGAACAAATGAGAGCTCAGATGTT 1863  
Db 484 rValProAsnLysAlaPheGluLysGluLysGluLysGluLysGluLysGluLysGluLys 504  
QY 1864 CCATCAGAAATCAAAACAAAGGAGATGAAGAAATCTTGGGATTCGAGAGTCCCTG 1923  
Db 504 eProProGluSerLysGlnLysAspTyrGluLysAsnSerTrpAspSerGluSerLeuCy 524  
QY 1924 TGAGACGGTTTCACAGAGGATGTGTATTTACCAAGCTCACATCAAAAGAAATTCGA 1983  
Db 524 sGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAs 544  
QY 1984 TACCTTAAGTGGAAATTAGAAGAGTCTCTTAAAGATGCTCTTCTGAGCCTACCTG 2043  
Db 544 pLysIleAsnGlyLysLeuGluGluSerProAsnLysAspGlyLeuLeuLysAlaThrCy 564  
QY 2044 TGGAAGGAAAGTTCTCTTCCAAATAAGCCTTAGAATTAAGGACAGAGAAACATTCAA 2103  
Db 564 sGlyMetLysValSerIleProThrLysAlaLeuGluLeuLysAspMetGlnThrPheLy 584  
QY 2104 AGCAGAGTCTCTGATTAAGATGCTCTTCTGAGCCTACCTGTGGAAGAAAGTTCTCT 2163  
Db 584 sAlaGluProProGlyLysProSerAlaPheGluPro 596  
QY 2164 TCCAAATAAGCCTTAGAATTAAGGACAGAGAAACACTCAAGAGAGTCTCCTGTATA 2223  
Db 597 597  
QY 2224 TGATGCTCTTCTGAAGCCTACTCTGGAAGAAAGTTCTCTTCCAAATAAGCTTAGA 2283  
Db 603 603  
QY 2284 ATTGAAGACAGAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGAAATCCAAACAAA 2343

Db 610 uLeuLysAsnGluGlnThrTrpArgAlaAspGluIleLeuProSerGluSerLysGlnLy 630  
QY 2344 GGATGATCAACAAATATCTTGGGATTTTGAGATTTCTTTCAGACTCTCTTACAGATGA 2403  
Db 630 sAspTyrGluLysAsnSerTrpAspThrGluSerLeuCysGluThrValSerGlnLysAs 650  
QY 2404 TGTGTGTTTATCCCAAGCTACACATCAAAAAGATTCGATACCTTAAGTGGAAATTAGA 2463  
Db 650 pValCysLeuProLysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGl 670  
QY 2464 AGACTCTCTCATAAAGATGCTCTTCTGAAGCCTACCTGTGGAATGAAAATTTCTCTCC 2523  
Db 670 uGlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIlePr 690  
QY 2524 AAAATAAGACCTTAGAATTAAGGACAGAGAAACATTCAAAAGCAGAGGATGTGAGTCTTGT 2583  
Db 690 oThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLys-- 709  
QY 2584 AGACTCCACATTCAGTCTTTTGGCAACCCGACTACTGAAAATTCACAGCTTACAAAAGT 2643  
Db 710 -ProSerAlaPhe 723  
QY 2644 TGAGGAAGACTTTAATCTTACTACCAAGGAGGAGCAACAAAGACACAGTAACTGGACAACA 2703  
Db 724 724  
QY 2704 GGAACGTGATTTGGCATTATTGACGAGCTCCACAGATCAACAAATAAGATGCCAC 2763  
Db 732 nGluGlnThrLeuArgAlaAspGluLeuPro 743  
QY 2764 ATCAGATTAGGAGAAAGAGATACAAAATCAACTTCAGATTCCTCAGATTATCTCTGT 2823  
Db 744 -SerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLysG 763  
QY 2824 GAGTATACACAGAAATTTATGAGTCTTACCTGAGGCTACATATCAAAAGAAATAAGAC 2883  
Db 763 uThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLy 783  
QY 2884 AACAAATCGCAAAATAGACAGTCT 2908  
Db 783 sIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysAr 803  
QY 2908 2908  
Db 803 gMetLysValSerIleProThrLysAlaLeuLeuLeuMetAspMetGlnThrPheLysAl 823  
QY 2909 -----CTGAAAGCCTTCTCAGTTTGAGCTGCCACTGAAATCAAACTCTGTCTCC 2961  
Db 823 aGluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPr 843  
QY 2962 AAATAAGCCTTAGAATGGAGAAATAAACAAACATTGAGAGCA 3004  
Db 843 oAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSe 863  
QY 3004 3004  
Db 863 rGluSerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluTh 883  
QY 3004 3004  
Db 883 rValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysI 903  
QY 3005 -----GATTCAACTACCTATCAAAATCTTGATGCTACTCTCTCTTG 3048  
Db 903 eSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCy 923  
QY 3049 TGAAGAGGAGGAGAACTTAAAGAGATTAACCTGTGAAACAAATACAGCAAAATAGAAACA 3108  
Db 923 sGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGl 943  
QY 3109 AATGAAAAATAGTTTGTGTACTACAAAGAACTGTGAGAGCGCAAGAAATATAATC 3168  
Db 943 nMetLysLysLysPheCysValLeuLysLysLysLysLysLysLysLysLysLysLys 963



QY 3169 ACAGTTAGAGAACCAAAAGCTAAATGGGAACAAGAGCTCTGACGTGTGAGATTGCCCTTT 3228  
 Db rGlnLeuGluAsnGlnLysValTyrTrpGluGlnGluLeuGluCysSerValArgLeuThrLe 983  
 QY 3229 AAATCAAGAGAGAGAGAGAGAAATGTCATATATTAAGAAAAATTTAGACCC-- 3286  
 Db uAsnGlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGlu 1003  
 QY 3287 -----GAAGACCACTTAGGAAAGTTAGAGTGAAGTGAACCACTTGAACA 3333  
 Db uLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeuGluGlu 1023  
 QY 3334 GACTCTCAGATACAGATATAGAAATGAAAGTGTAAACAGTAATTTGAATCAGGTTTC 3393  
 Db nalaLeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSe 1043  
 QY 3394 TCACATCATGAAGTGAATGATCTCTTTCATGAAATTCGATGTTGAAAGAGAAAT 3453  
 Db rHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluL 1063  
 QY 3454 TGCATGCTAAACTGGAAGTAGCCACACTGAACATCAACACAGGTGAAGGAAATAA 3513  
 Db ealaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLy 1083  
 QY 3514 ATACTTTGAGGACATTAAGATTTTACAGAAAGAGATGCTGAACCTCAAAAGACCTTAA 3573  
 Db sTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLy 1103  
 QY 3574 ACTGAACAGAAACAGTAAACAAAGGCGCTCTCAGTATAGAGAGCAGCTTAAAGTTCT 3633  
 Db sLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValle 1123  
 QY 3634 GACGCGAGAGAACACAGTCTGACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3673  
 Db uIleAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 1136

RESULT 9  
 ABUJ37783  
 ID ABUJ37783 standard; protein; 1013 AA.  
 AC ABUJ37783;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE Human tumour-related protein - SEQ ID NO 553.  
 XX  
 KW Human; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 KW tumour; breast cancer; cancer; immune response stimulation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200283956-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 15-APR-2002; 2002WO-US012378.  
 XX  
 PR 13-APR-2001; 2001US-00834759.  
 PR 07-DEC-2001; 2001US-00007805.  
 PR 13-FEB-2002; 2002US-00076622.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;  
 PI Vedvick TS, McNeill PD, Durham M;  
 XX  
 DR WPI; 2003-103376/09.  
 XX  
 PT New polypeptide and polynucleotide useful for stimulating and/or  
 PT expanding T cells specific for a tumor protein and treating breast  
 PT cancer.

XX PS  
 XX CC The invention comprises a method of stimulating and/or expanding T cells  
 CC specific for a tumor protein. The invention further comprises human  
 CC nucleic acids and proteins that are associated with tumors (e.g. breast  
 CC cancer). The method and sequences of the invention are useful for  
 CC stimulating and/or expanding T cells specific for a tumor protein,  
 CC detecting the presence of cancer, stimulating an immune response in a  
 CC patient and treating breast cancer. The present amino acid sequence  
 CC represents a human tumour-related protein  
 XX  
 SQ Sequence 1013 AA;  
 Alignment Scores: Length: 1013  
 Pred. No.: 8,59e-185 Matches: 512  
 Score: 2374.00  
 Percent Similarity: 62.62% Conservative: 61  
 Best Local Similarity: 55.96% Mismatches: 126  
 Query Match: 36.82% Indels: 216  
 DB: 6 Gaps: 9  
 US-09-602-362E-26 (1-3673) x ABUJ37783 (1-1013)  
 QY 1199 TTGAGGCTACAAAAGAAACATCTGAGAAATTTTCATGCGCAGCAAAAGAAATCTAGG 1258  
 Db 12 MetSerProAlaLysGluThrSerGluLysPheThrTrpAlaAlaLysGlyArgProArg 31  
 QY 1259 AAGATCATCATCGGAGGAGAAAGAAACATCTGTAAGACTGAATGCGTGGCAGGAGTAA 1318  
 Db 32 LysIleAlaTrpGluLysLysGluThrProValLysThrGlyCysValAlaArgValThr 51  
 QY 1319 CCTAATAAACTGAAGTTTGGAAAAAGGAACATCTAATATGATTCATGCTCTCAAAA 1378  
 Db 52 SerAsnLysThrLysValLeuGluLysGlyArgSerLysMetIleAlaCysP-ProThrLys 71  
 QY 1379 GAAACATCTCAAAAGCAAGTACAAATGCGGATGCGATGCTCTGAGAGCTATTTACGT 1438  
 Db 72 GluSerSerThrLysAlaSerAlaAsn----- 80  
 QY 1439 CTTTTTGCACACGCGACTATTGAAAAATTACAGTGTACAAAAGTTGAGGAAGACTTTAAT 1498  
 Db 80 ----- 80  
 QY 1499 CTTGCTACCAAGATATCTCTAAGAGTGTGCGACAGAAATTATAGTGTTTACCTGATGCT 1558  
 Db 80 ----- 80  
 QY 1559 ACATATCAAAAAGATATCAAAAACAATAAATCACAAAATAGAGATCAGATGTTCCCATCA 1618  
 Db 81 -----AspGlnArgPheProSer 86  
 QY 1619 GAATCCAAAACGAGAGAGAGATGAAGAATATTCTGGGATCTGGGAGCTCTCTTTGAGAGT 1678  
 Db 87 GluSerLysGlnGluGluAspGluLysTrpSerCysAspSerArgSerLeuPheGluSer 106  
 QY 1679 TCTGCAAGACTCAAGTGTGTATACCTGAGTGTATGATATGATATGATATGATATGATAT 1738  
 Db 107 SerAlaLysIleGlnValCysIleProGluSerIleTyrGlnLysValMetGluIleAsn 126  
 QY 1739 AGAGAAGTAGAAGAGCTTCTCTGAGAGCCATCTGCTTCAAGCTCGCGTNGAAATGCAA 1798  
 Db 127 ArgGluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGln 146  
 QY 1799 AAGACTGTTCCAAATAAAGCTTTGAATTTGAGATGAAGATGAAGATGAAGATGAAGAT 1858  
 Db 147 AsnSerValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAspPro 166  
 QY 1859 ATGTTTCCCATCAGAAATCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1918  
 Db 167 MetPheProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSer 186  
 QY 1919 CCCTGTGAGACGGTTTTCACAGAGAGTGTGTATTATCCCAAGCTACATCAAAAGAA 1978



Db 187 LeuCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGlu 206  
QY 1979 TTCGATACCTTAAGTCGAAATTAAGAGAGTCTCTGTTAAAGATGCTTCTTGAAGCCT 2038  
Db 207 IleAspLysIleAsnGlyLysLeuGluGluSerProAsnLysAspGlyLeuLeuLysAla 226  
QY 2039 ACTGTGAGGAAGAAGTTCTCTTCCAAATAAAGCTTAGAATTAAAGGACAGACAGAAACA 2098  
Db 227 ThrCysGlyMetLysValSerIleProThrLysAlaLeuGluLeuLysAspMetGlnThr 246  
QY 2099 TTCAAAGCAGAGTCTCTGATAAAGATGCTCTCTGAAAGCTTACCTGTGGAAGGAAGTT 2158  
Db 247 PheLysAlaGluProProGlyLysProSerAlaPheGluProAlaThrGluMetGlnLys 266  
QY 2159 TCTCTTCCAAATAAAGCCTTAGAATTAAGGACAGACAGAACTCAAGCAGAGTCTCT 2218  
Db 267 SerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAsp----- 284  
QY 2219 GATAATGATGCTCTCTGAGCCTACCTGTGGAAGGAAGTTCTCTTCCAAATAAAGCT 2278  
Db 284 ----- 284  
QY 2279 TTAGAATTGAAGCAGACAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGAAATCCAAA 2338  
Db 285 -----GluIleLeuProSerGluSerLys 292  
QY 2339 CAAAGGATGATGAAGAAATCTTGGGATTTTGAGAGTTTCCCTTGAGACTCTCTTACAG 2398  
Db 293 GlnLysAspTyrGluGluAsnSerTrpAspThrGluSerLeuCysGluThrValSerGln 312  
QY 2399 AATGATGTGTGTTACCCAGGCTACATCAAAAAGAAATTCGATACCTTAAGTGGAAA 2458  
Db 313 LysAspValCysLeuProLysAlaLahisGlnLysGluIleAspLysIleAsnGlyLys 332  
QY 2459 TTAGAAGAGTCTCTGATTAAGATGGTCTTCTGGAAGCCTACTCTGGAATGAATTTCT 2518  
Db 333 LeuGluGlySerProGlyLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSer 352  
QY 2519 CTTCCAAATAAAGCCTTAGAATTGAAGCAGACAGAAACATTCAAAGCAGAGGATCTGAGT 2578  
Db 353 IleProThrLysAlaLeuGluLeuValAspMetGlnThrPheLysAlaGluProProGlu 372  
QY 2579 TCTGAGAGTCCACATTCAGTCTTTTGGCAACCGACTACTGAAATTCACAGTCTACA 2638  
Db 373 Lys---ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal 387  
QY 2639 AAAGTTGAGGAGACTTTAATCTTACTACAGGAGGAGGACAAACAGACAGTAACTGGA 2698  
Db 388 -----ProAsnLysAlaLeuGluLeu 394  
QY 2699 CAACAGGAACGTGATATTGGCATTATTGAACGAGCTCCACAAAGATCAACAAATAAGATG 2758  
Db 395 LysAsnGluGlnThrLeuArgAlaAspGluIleLeuPro----- 407  
QY 2759 CCCATCAGAAATTAGGAAGAAAGAGATACAAATCAACTTCAGATTCGAGATATC 2818  
Db 408 -----SerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLys 425  
QY 2819 TCTGTGAGTATACACAGAAATTTAGTGTTTACTCTGAGGCTACATATCAAAAAGAAATA 2878  
Db 426 CysGluThrValSerGlnLysAspValCysLeuProLysAlaLahisGlnLysGluIle 445  
QY 2879 AAGACAAATAAGGCAAAATGAAGAGTCT----- 2908  
Db 446 AspLysIleAsnGlyLysLeuGluGluSerProAsnAspGlyPheLeuLysSerPro 465  
QY 2908 ----- 2908  
Db 466 CysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPhe 485  
QY 2909 -----CCTGAAAGCCTTCTCAGCTTTCAGCTGCGCTGCAATGCAAACTCT 2956  
|||||

Db 486 LysAlaGluProProGluLysProSerAlaPheGluProAlaThrLeuMetGlnLysSer 505  
QY 2957 GTTCCAAATAAAGCCTTAGAATGAAGATAAACAACATTCAGAGCA----- 3004  
Db 506 ValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPhe 525  
QY 3004 ----- 3004  
Db 526 ProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSerLeuArg 545  
QY 3004 ----- 3004  
Db 546 GluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAsp 565  
QY 3005 -----GATTCAACTACCCTATCAAAAATCTTGGATGACACTTCCT 3043  
Db 566 LysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHis 585  
QY 3044 TCTTGTCAAGAGAGGGAACCTTAAAGAAGATACTGTGAACAAATTCACAGCAAAATG 3103  
Db 586 SerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMet 605  
QY 3104 GAACAAATGAAAAATAAGTTTTGTACTACAAAAGGAAGCTGTCAAGAGCAAAAGAAATA 3163  
Db 606 GluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIle 625  
QY 3164 AATCAGAGTTAGAGAACCAAAAGCTAAATCGGAACAGAGCTCTGCAGTGTGAGATTG 3223  
Db 626 LysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLeuCysSerValA-gLeu 645  
QY 3224 CCTTTAAATCAGAAGAAGAGAGAGAAATGTCGATATATTAAAAAGAAAAATAGGA 3283  
Db 646 ThrLeuAsnGlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArg 665  
QY 3284 CCC-----GAAGAGCAACTTAGAAAAAGTTAGAGTGAACCAACTT 3328  
Db 666 GluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeu 685  
QY 3329 GAACAGACTCTCAGAAATACAAAGATATAGAAATTCGAAAGTCAACAAAGTAAATTTGAATCAG 3388  
Db 686 GluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGln 705  
QY 3389 GTTCTCAGACTCATGAAAGTGAATGATCTCTTTTCATGAAAAATTCATGTTTGAAGAAAG 3448  
Db 706 ValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLys 725  
QY 3449 GAAATTCCTCATGTAAGTGGAGTAGCCACACTGAACATCAACACAGGTGAAGGAA 3508  
Db 726 GluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGlu 745  
QY 3509 AATAAATACCTTTGAGGACATTAAGATTTTACAAAGAAAAAGAAATCTGCAACTTCAAAATGACC 3568  
Db 746 AsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThr 765  
QY 3569 CTAAACTGAAACAGAAACAGTAACAAAAGGGCATCTCAGTATAGAGAGAGCTTAA 3628  
Db 766 LeuLysLeuLysGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLys 785  
QY 3629 GTTCTCAGCGCACAGAACGATGCTGACTTCTTAAATTTGAAGCAA 3673  
Db 786 ValIleAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 800  
RESULT 10  
AAU33357  
ID AAU33357 standard; protein; 1095 AA.  
XX AC AAU33357;  
XX DT 18-DEC-2001 (first entry)  
XX DE Human breast cancer protein B726P fusion protein #1.  
XX KW Human; ss; breast cancer protein; tumour; cancer; cytostatic;

KW gene therapy; immunogen.  
 XX Homo sapiens.  
 XX WO200179286-A2.  
 PN 25-OCT-2001.  
 XX 12-APR-2001; 2001WO-US012164.  
 XX 17-APR-2000; 2000US-00551621.  
 PR 08-JUN-2000; 2000US-00590751.  
 PR 22-JUN-2000; 2000US-00604287.  
 PR 20-JUL-2000; 2000US-00620405.  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;  
 PI WPI; 2001-611721/70.  
 DR N-PSDB; AAS47421.  
 XX  
 PT Breast Tumor Proteins and nucleic acids useful for the prevention,  
 PT diagnosis and treatment of breast cancer.  
 XX  
 PS Claim 22; Page 292-295; 297pp; English.  
 XX  
 CC The invention relates to isolated breast tumour proteins and nucleic  
 CC acids that encode them, including immunogenic fragments of the proteins.  
 CC Also included are expression vectors expressing the proteins, transformed  
 CC cells and antibodies raised against the proteins or an antigen presenting  
 CC cell expressing the protein. The proteins and nucleic acids may be used  
 CC in the prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate breast tumour protein expression, i.e. breast tumours and  
 CC breast cancer e.g by gene therapy. The nucleic acids and their  
 CC complements may also be used as DNA probes in diagnostic assays to detect  
 CC and quantitate the presence of similar nucleic acids in samples, and  
 CC therefore which patients may be in need of restorative therapy. The  
 CC proteins, nucleic acids and antibodies may be used in assays to identify  
 CC modulators (e.g. antagonists) of breast tumour protein expression and  
 CC activity. The antibodies and antagonists may also be used to down  
 CC regulate expression and activity. The antibodies may also be used as  
 CC diagnostic agents for detecting the presence of the proteins in samples  
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-  
 CC purification diagnostic techniques. The present sequence is a breast  
 CC tumour protein encoded by a cDNA from a breast tumour cDNA library  
 CC isolated by subtractive hybridisation against a normal breast cDNA  
 CC library  
 XX  
 SQ Sequence 1095 AA;

Alignment Scores:  
 Pred. No.: 1,18e-184 Length: 1095  
 Score: 2372.50 Matches: 529  
 Percent Similarity: 59.37% Conservative: 73  
 Best Local Similarity: 52.17% Mismatches: 151  
 Query Match: 36.79% Indels: 261  
 DB: 4 Gaps: 13

US-09-602-362E-26 (1-3673) x AAU33357 (1-1095)

QY 950 CTTTTCGACATATACGAAATTTACCTAAATAATCCATCCAGAGAACCA 1009  
 |||||:|||||:  
 Db 24 LeuLeuGluAsnValIleSerLysThrIleAsnProGlnValSerLysThrGlu----- 41  
 |||||:|||||:  
 QY 1010 TCTACAGGACACCTGATGAGGTGACCCCTTGGCGGAGAGAACACCTGACACGCTGAA 1069  
 |||||:|||||:  
 Db 42 -----TyrLys 43  
 |||||:|||||:  
 QY 1070 AGCTTCTGGAATAACACCTGACGAGGTGACCGCTTGGTGGAGGACGCTCTGCCAAA 1129  
 |||||:|||||:  
 Db 44 GluLeuGlnGluPheIleAspAsnAla-----ThrThrAsnAla 58  
 |||||:|||||:

QY 1130 ATTCAATGTCGGGAAAGCAACATCTGGAAGTGTGAAACAGTCAACACAGAAACACCT 1189  
 |||||:|||||:  
 Db 59 IleAspGluLeuLysGluCys-----PheLeuAsnGlnThrAspGluThrLeu 74  
 |||||:|||||:  
 QY 1190 AGGAAATTT-----TTG 1201  
 |||||:|||||:  
 Db 75 SerAsnValGluValPheMetGlnLeuIleTyrAspSerSerLeuCysAspLeuPheMet 94  
 |||||:|||||:  
 QY 1202 AGCCTACAAAGAAACATCTGAGAAATTTTCATGCCAGCAAGAAAGAAAGATCTAGGAG 1261  
 |||||:|||||:  
 Db 95 SerProAlaLysGluThrSerGluLysPheThrTrpAlaAlaLysGlyArgProArgLys 114  
 |||||:|||||:  
 QY 1262 ATCACAATGGGAGGAAAGAAACATCTGTAAGACATGAATGCGTGGCAGGATTAACACCT 1321  
 |||||:|||||:  
 Db 115 IleAlaTrpGluLysGluThrProValLysThrGlyCysValAlaArgValThrSer 134  
 |||||:|||||:  
 QY 1322 AATAAACTGAAGTCTTTGAAAGAAAGCAATCTTAATATGATTCATGTCATCTCTCAAAAGAA 1381  
 |||||:|||||:  
 Db 135 AsnLysThrLysValLeuGluLysGlyArgSerLysMetIleAlaCysProThrLysGlu 154  
 |||||:|||||:  
 QY 1382 ACATCTACAAAGCAAGTACAAATGTGGATGTGAGTCTCTGTAGAGCCTATATTCAGTCTT 1441  
 |||||:|||||:  
 Db 155 SerSerThrLysAlaSerAlaAsn----- 162  
 |||||:|||||:  
 QY 1442 TTTGGCACCGGACTATTGAAATTCACAGTGTACAAAGTTTTCAGGAGACTTTAATCTT 1501  
 |||||:|||||:  
 Db 162 ----- 162  
 |||||:|||||:  
 QY 1502 GCTACCAAGATTATCTTAAGAGTGTGCACAGAATTACGTGTACGTGATGCTACA 1561  
 |||||:|||||:  
 Db 162 ----- 162  
 |||||:|||||:  
 QY 1562 TATCAAAAGATATCAAAACAATAATCAAAATAGAAGATCAGATGTTCCCATCAGAA 1621  
 |||||:|||||:  
 Db 163 -----AspGlnArgPheProSerGlu 169  
 |||||:|||||:  
 QY 1622 TCCAAACGAGAGGAGAGTAAAGTATTTCTGGAGTCTGGGAGTCTCTTTCAGAGTCTT 1681  
 |||||:|||||:  
 Db 170 SerLysGlnGluAspGluGluTyrSerCysAspSerArgSerLeuPheGluSerSer 189  
 |||||:|||||:  
 QY 1682 GCAAGACTCAAGTGTATACCTGATCTATCTATCAGAAAGTAAATGAGATTAATAGA 1741  
 |||||:|||||:  
 Db 190 AlaLysIleGlnValCysIleProGluSerIleTyrGlnLysValMetGluIleAsnArg 209  
 |||||:|||||:  
 QY 1742 GAAGTACAGAGCTCTCTGAGAGCCATCTGCTTCAAGCCTCCCTGNGAATTCGAAAG 1801  
 |||||:|||||:  
 Db 210 GluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGlnAsn 229  
 |||||:|||||:  
 QY 1802 ACTGTTCCAAATAAGCCTTTGAATTGAAGATGAACAAACATTGAGACAGCTCAGATG 1861  
 |||||:|||||:  
 Db 230 SerValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAspProMet 249  
 |||||:|||||:  
 QY 1862 TTCCCATCAGATCCAAACAAAGAGCAGATGAAGAAATTTCTTTGGGATTTCTGAGAGTCCC 1921  
 |||||:|||||:  
 Db 250 PheProGluSerLysGlnLysAspTyrGluAsnSerTrpAspSerGluSerLeu 269  
 |||||:|||||:  
 QY 1922 TGTGAGACGGTTTACAGAGAGTGTGATTTTACCACCAAGCTACATCAAAAGAAATTC 1981  
 |||||:|||||:  
 Db 270 CysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIle 289  
 |||||:|||||:  
 QY 1982 GATACCTTAAGTGGAAATTTAGAGAGTCTCCCTGTTAAAGATGCTCTTCTGAAGCCTACC 2041  
 |||||:|||||:  
 Db 290 AspLysIleAsnGlnLysLeuGluSerProAsnLysAspGlyLeuLeuLysAlaThr 309  
 |||||:|||||:  
 QY 2042 TGTGGAAGGAAAGTTCTCTTCCAAATAAGCCTTTAGAAATTAAGGACAGAGAAACATTC 2101  
 |||||:|||||:  
 Db 310 CysGlyMetLysValSerIleProThrLysAlaLeuGluLeuLysAspMetGlnThrPhe 329  
 |||||:|||||:  
 QY 2102 AAAGCAGGTCTCTGATTAAGATGGTCTTCTCAAGCCTACCTGTGTGAAGAAAGTTTCT 2161  
 |||||:|||||:  
 Db 330 LysAlaGluProProGluLysProSerAlaPheGluProAlaThrGluMetGlnLysSer 349  
 |||||:|||||:  
 QY 2162 CTTCCAAATAAGCCTTAGAATTTAAAGGACAGAGAAACACTCAAGACAGAGTCTCTGAT 2221  
 |||||:|||||:



PR 22-JUN-2000; 2000US-00604287.  
 PR 20-JUL-2000; 2000US-00620405.  
 XX  
 XX (CORI-) CORIXA CORP.  
 XX Jiang Y. Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT,  
 PI Henderson RA;  
 PI  
 XX WPI; 2002-635657/68.  
 DR N-PSDB; ABS64022.  
 XX  
 XX Novel breast cancer polynucleotides and polypeptides encoded by the  
 PT polynucleotides, useful for detecting the presence of breast cancer in a  
 PT patient, and in pharmaceutical compositions, for treating breast cancer.  
 XX  
 PS Disclosure; Page 223-225; 247pp; English.  
 XX  
 CC The invention relates to an isolated breast tumour polynucleotide and the  
 CC polypeptide it encodes. The polynucleotide and polypeptide are useful for  
 CC detecting the presence of breast cancer in a patient, and in  
 CC pharmaceutical compositions for treating breast cancer. The sequences are  
 CC useful for stimulation of an immune response in a patient and can therefore  
 CC be used in production of vaccines. The sequences are also useful for  
 CC detecting the presence of a cancer in a patient, by obtaining a  
 CC biological sample from the patient, contacting the biological sample with  
 CC a composition of the invention and detecting the amount of polynucleotide  
 CC that hybridizes to the sample. This sequence represents a human breast  
 CC tumour polypeptide of the invention  
 XX  
 XX Sequence 1095 AA;  
 SQ

Alignment Scores:  
 Pred. No.: 1,18e-184 Length: 1095  
 Score: 2372.50 Matches: 529  
 Percent Similarity: 59.37% Conservative: 73  
 Best Local Similarity: 52.17% Mismatches: 151  
 Query Match: 36.79% Indels: 261  
 DB: 5 Gaps: 13

US-09-602-362E-26 (1-3673) x ABG78924 (1-1095)  
 QY 950 CTTTGGACATATACGAAATACCTAAATCTCTAAATACCAATCCAGAGGAACA 1009  
 Db  
 24 LeuLeuGluAsnValIleSerLysThrIleAsnProGlnValSerLysThrGlu----- 41  
 QY 1010 TCTACAGGAACACCTGATGAGGCTGCACCTTTGGCGAAGAAACACCTGCACAGCGCTGAA 1069  
 Db  
 42 -----TyrLys 43  
 QY 1070 AGCTTCTGGAAAAACACCTGACGAGGCTGCACGCTTGGTGGGAGGACGCTGCCCAA 1129  
 Db  
 44 GluLeuLeuGlnGluPheIleAspAspAsnAla-----ThrThrAsnAla 58  
 QY 1130 ATTCAATGTCTGGGAAAGCAACATCTGGAAGAGTTTGAACAGCTCAACAGAGAAACACCT 1189  
 Db  
 59 IleAspGluLeuLysGluCys-----PheLeuAsnGlnThrAspGluThrLeu 74  
 QY 1190 AGGAAATTT-----TTG 1201  
 Db  
 75 SerAsnValGluValPheMetGlnLeuIleTyrAspSerSerLeuCysAspLeuPheMet 94  
 QY 1202 AGCGCTACAAAGAAACATCTGAGAAATTTTCATGCCAGCAAAAGAAAGATCTAGGAAG 1261  
 Db  
 95 SerProAlaLysGluThrSerGluLysPheThrTyrAlaAlaLysGlyArgProArgLys 114  
 QY 1262 ATCAGATGGAGAGAAAGAAACATCTGTAAGACCTGAATGCGTGGCGAGGATACACCT 1321  
 Db  
 115 IleAlaTyrGluLysLysGluThrProValLysThrGlyCysValAlaArgValThrSer 134  
 QY 1322 AATAAACCTGAGTTTGGAAAGAAACATCTAATATGATGTCCTTCAACAAAGAA 1381  
 Db  
 135 AsnLysThrLysValLeuGluLysGlyArgSerLysMetIleAlaCysProThrLysGlu 154

QY 1382 ACATCTACAAAGCAAGTACAAATGTGGATGTGAGTTCTGTAGAGCCTATATTACTCTT 1441  
 Db  
 155 SerSerThrLysAlaSerAlaAsn----- 162  
 QY 1442 TTTGGCACCGGACTATTGAAATTCACAGTGTACAAAAGTTGAGGAACACTTTAATCTT 1501  
 Db  
 162 ----- 162  
 QY 1502 GCTACCAAGATTATCTTAAGAGTGTGCACAGATTATACGTTTACTCTGATGCTACA 1561  
 Db  
 162 ----- 162  
 QY 1562 TATCAAAAAGATATCAAAACAATAAATCAAAAATAGAAGATCAGATGTTCCCATCAGAA 1621  
 Db  
 163 -----AspGlnArgPheProSerGlu 169  
 QY 1622 TCCAAACGAGGAGAGTGAAGTATCTTGGGATCTCTGGGAGTCTCTTTGAGAGCTCT 1681  
 Db  
 170 SerLysGlnGluAspGluGluTyrSerCysAspSerArgSerLeuPheGluSerSer 189  
 QY 1682 GCAAAAGACTCAAGTGTCTATACCTGAGTCTATGTATCAGAAAAGTAAATGAGATAAATAGA 1741  
 Db  
 190 AlaLysIleGlnValCysIleProGluSerIleTyrGlnLysValMetGluIleAsnArg 209  
 QY 1742 GAAGTAGAAGAGCTTCTGAGAGAGCCTGCTTCAAGCCTCCGCTGAAATGCAAAAG 1801  
 Db  
 210 GluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGlnAsn 229  
 QY 1802 ACTGTTCCAAATAAAGCCTTTGAATTTGAAGATGAACAAACATTTGAGAGCAGCTCAGATG 1861  
 Db  
 230 SerValProAsnLysAlaPheGluLeuLysAsnGlnThrLeuArgAlaAspProMet 249  
 QY 1862 TTCCCATCAAGATCCAAACAAAGAGCGATGAAGAAAATTTCTGGGATCTCTGAGATGCC 1921  
 Db  
 250 PheProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSerLeu 269  
 QY 1922 TGTGAGACGGTTTCCAGAGAGGATGTATTATCCCAAGCTACACATCAAAAGAAATTC 1981  
 Db  
 270 CysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIle 289  
 QY 1982 GATACCTTAAAGTGAAGATTTAGAGAGTCTCTGTTAAAGATGGTCTTTGAGAGCCTACC 2041  
 Db  
 290 AspLysIleAsnGlyLysLeuGluSerProAsnLysAspGlyLeuLeuLysAlaThr 309  
 QY 2042 TGTGGAAGGAAAGTTCTCTCCAAATTAAGCCTTAGAATTAAGGACAGAGAAACATTC 2101  
 Db  
 310 CysGlyMetLysValSerIleProThrLysAlaLeuGluLeuLysAspMetGlnThrPhe 329  
 QY 2102 AAAGCAGAGTCTCTGATAAAGATGGTCTTCTGAAGCCTACCTGTGGAAGAAAGTTTCT 2161  
 Db  
 330 LysAlaGluProGlyLysProSerAlaPheGluProAlaThrGluMetGlnLysSer 349  
 QY 2162 CTTCCAAATTAAGCCTTAGAATTAAGGACAGAGAAACACTCAAGACAGAGTCTCTGAT 2221  
 Db  
 350 ValProAsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAsp----- 366  
 QY 2222 AATGATGCTCTCTGGAAGCCTACCTGTGGAAGGAAAGTTTCTCTCCAAATAAAGCTTTA 2281  
 Db  
 366 ----- 366  
 QY 2282 GAATTGAGGACAGAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGAAATCCAAACA 2341  
 Db  
 367 -----GluIleLeuProSerGluSerLysGln 375  
 QY 2342 AAGGATGATCAAGAAATTTCTGGGATTTTGAGAGTTTCTCTGAGACTCTCTTACAGAAT 2401  
 Db  
 376 LysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLys 395  
 QY 2402 GATGTGTGTTTACCAGGCTACACATCAAAAGAAATTCGATACCTTAAGTGGAAATTA 2461  
 Db  
 396 AspValCysLeuProLysAla\*\*\*HisGlnLysGluIleAspLysIleAsnGlyLysLeu 415  
 QY 2462 GAAGAGTCTCTGATTAAGATGCTCTCTGAAACCTACCTGTGGAAGTGAATGAAATTTCTCTT 2521

Db 416 GluGlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIle 435  
 QY 2522 CCAATTAAGCCCTTGAATTTGAAGACACAGAGAAACATTCAAGCAGAGAGATGTGAGTTCT 2581  
 Db 436 ProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLys 455  
 QY 2582 GTAGAGTCCACATTCAGTCTTTTGGCAAAACCGACTACTCTGAAAAATTCACAGTCTACAAA 2641  
 Db 456 ---ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal--- 469  
 QY 2642 GTTAGGAGAGACTTTAACTTACTACCAAGGAGGAGCAACAAGACAGTAACTGGACAA 2701  
 Db 470 -----ProAsnLysAlaLeuGluLys 477  
 QY 2702 CAGGAACGTGATTTGGCATTATTGAACGAGCTCCACCAAGATCAAAACAATAAGATGCC 2761  
 Db 478 AsnGluGlnThrLeuArgAlaAspGluIleLeuPro----- 489  
 QY 2762 ACATCAGATTAAGGAAGAAAGAAATCAAAATCACTTCAGATTCAGATTCATCTCT 2821  
 Db 490 ---SerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys 508  
 QY 2822 GTGAGTGATACACAGAAATATCAGTGTTTACCTGAGGCTACATATCAAAAAGAAATAAAG 2881  
 Db 509 GluThrValSerGlnLysAspValCysLeuProLysAla\*\*HisGlnLysGluIleAsp 528  
 QY 2882 ACACAAAATGGCAAAATAGAAGAGTCT----- 2908  
 Db 529 LysIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCys 548  
 QY 2908 ----- 2908  
 Db 549 ArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLys 568  
 QY 2909 -----CCTGAAAGCCTTCTCATTGTGAGCCTGCCTGAAATGCAAACTCTCTT 2959  
 Db 569 AlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerVal 588  
 QY 2960 CCAATTAAGGCTTGAATGGAAGATAAACAACATTGAGAGCA----- 3004  
 Db 589 ProAsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPhePro 608  
 QY 3004 ----- 3004  
 Db 609 SerGluSerLysGlnLys\*\*ValGluGluAsnSerTrpAspSerGluSerLeuArgGlu 628  
 QY 3004 ----- 3004  
 Db 629 ThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLys 648  
 QY 3005 -----GATTCACTACCTTATCAAAAATCTTGATGCACTTCTTCT 3046  
 Db 649 IleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSer 668  
 QY 3047 TGTGAAAGAGGAGGAACTTAAAGAAATGATCTGCAACAAATTTACAGCAAAATGAA 3106  
 Db 669 CysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGlu 688  
 QY 3107 CAAATGAAATAAGTTTGTCTACTACAAAGGAAGTCTCAGAGCCGAAGAATAAAA 3166  
 Db 689 GlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLys 708  
 QY 3167 TCACAGTTAGAGAACCAAAAGCTAAATGGGAACCAAGAGCTCTGAGTGTGAGATTGCT 3226  
 Db 709 SerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuLysSerValArgLeuThr 728  
 QY 3227 TTAATTAAGAGAGAGAGAGAGAAATGTGATATATTAAAGAAAAATAGACCC 3286  
 Db 729 LeuAsnGlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGlu 748  
 QY 3287 -----CAGAGCAACTTAGGAAAGATTAGAGTCAACACCAACTTCAA 3331

Db 749 GluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlu 768  
 QY 3332 CAGACTCTCAGATACAGATATAGAAATTCGAAAGTGTAACAAGTAATTTCAATCAGGTT 3391  
 Db 769 GlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnVal 788  
 QY 3392 TCTCAGACTCATGAAAGTGAATGATCTCTTTCATGAAAAATTCGATGTTGAAAAAGGAA 3451  
 Db 789 SerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGlu 808  
 QY 3452 ATTGCCATGCTAAACCTGGAGTAGCCACACTCAAAACATCAACACAGGTGAAGGAAAT 3511  
 Db 809 IleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnIleGlnGluLysGluAsn 828  
 QY 3512 AAATACTTTGAGGACATTAAGATTTTACAGAAAAAGAAATGCTCAACTTCAAAATGACCTTA 3571  
 Db 829 LysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeu 848  
 QY 3572 AAATGAAACAGAAACAGTAACAAAAGGGCATCTCAGTATAGAGAGAGAGCTTAAAGTT 3631  
 Db 849 LysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysVal 868  
 QY 3632 CTGACGGCAGACACACGATGCTGACTTCTAAATTTGAAGGAA 3673  
 Db 869 LeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 882  
 RESULT 12  
 ABJ37747  
 ID ABJ37747 standard; protein; 1095 AA.  
 XX AC ABJ37747;  
 XX DT 15-MAY-2003 (first entry)  
 DE Human tumour-related protein - SEQ ID No 493.  
 KW Human; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 KW tumour; breast cancer; cancer; immune response stimulation.  
 OS Homo sapiens.  
 XX WO200283956-A1.  
 XX PD 24-OCT-2002.  
 XX PF 15-APR-2002; 2002WO-US012378.  
 XX PR 13-APR-2001; 2001US-00834759.  
 XX PR 07-DEC-2001; 2001US-00007805.  
 XX PR 13-FEB-2002; 2002US-00076622.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;  
 PI Vedvick TS, McNeill PD, Durham M;  
 XX WPI; 2003-103376/09.  
 PT New polypeptide and polynucleotide useful for stimulating and/or  
 PT expanding T cells specific for a tumor protein and treating breast  
 XX cancer.  
 XX PS Disclosure; Page 310-312; 375pp; English.  
 CC The invention comprises a method of stimulating and/or expanding T cells  
 CC specific for a tumour protein. The invention further comprises human  
 CC nucleic acids and proteins that are associated with tumours (e.g. breast  
 CC cancer). The method and sequences of the invention are useful for  
 CC stimulating and/or expanding T cells specific for a tumour protein,  
 CC detecting the presence of cancer, stimulating an immune response in a  
 CC patient and treating breast cancer. The present amino acid sequence  
 CC represents a human tumour-related protein

XX SQ Sequence 1095 AA;

Alignment Scores:

Pred. No.:	1-18e-184	Length:	1095
Score:	2372.50	Matches:	529
Conservative:	59.37%	Mismatches:	73
Best Local Similarity:	52.17%	Indels:	261
Query Match:	36.79%	Gaps:	13

DB: 6

US-09-602-362E-26 (1-3673) x ABJ37747 (1-1095)

QY 950 CTTTTCGACATACGAAATTTACCTAAATCTCCTCAATACCAATCCAGAGGAACA 1009

DB 24 LeuLeuGluAsnValIleSerLysThrIleAsnProGlnValSerLysThrGlu-----41

QY 1010 TCTACAGGAACACCTGATGAGGCTGCACCCCTGGCGAAAGAACACCTGACACGGCTGAA 1069

DB 42 -----TyrLys 43

QY 1070 AGCTTCTGGAACAAACACCTGACGAGGCTGCACGGCTTGGTGAGGAAGCTCTGCCAAA 1129

DB 44 GluLeuLeuGlnGluPheIleAspAspAsnAla-----ThrThrAsnAla 58

QY 1130 ATTCAATGTCTGGGAAAGCAACATCTGGAAAGTTTGAACAGTCAACAGAGAAACACCT 1189

DB 59 IleAspGluLeuLysGluCys-----PheLeuAsnGlnThrAspGluThrLeu 74

QY 1190 AGGAAAT-----TTG 1201

DB 75 SerAsnValGluValPheMetGlnLeuIleTyrAspSerSerLeuCysAspLeuPheMet 94

QY 1202 AGCCCTACAAAGAACATCTGGAATTTTCATGCCCGCAAGAAAGATCTAGGAG 1261

DB 95 SerProAlaLysGluThrSerGluLysPheThrTrpAlaLysGlyArgProArgLys 114

QY 1262 ATCACATGGAGAGAAAGAAACATCTGTAAGACTGAATGGTGGCGAGGATACACCT 1321

DB 115 IleAlaTrpGluLysLysGluThrProValLysThrGlyCysValAlaArgValThrSer 134

QY 1322 AATAAATCGAAGTTTGGAAAGAACATCTAATATGATGTCATCTCTACAAAGAA 1381

DB 135 AsnLysThrLysValLeuGluLysGlyArgSerLysMetIleAlaCysProThrLysGlu 154

QY 1382 ACATCTACAAAGCAAGTACAAATGTGGATGTGAGTTCTGTAGAGCCTATATTCAGTCT 1441

DB 155 SerSerThrLysAlaSerAlaSer-----162

QY 1442 TTTGGCACACGGACTATTGAAATTCACAGTGTACAAAGTTGAGGAGACTTTTAACTTT 1501

DB 162 -----162

QY 1502 GCTACCAAGATTATCTTAAGAGTGTGCACAGAAATTATACGTGTTTACCTGATGCTACA 1561

DB 162 -----162

QY 1562 TATCAAAAAGATATCAAAAACAATAAATCAAAAATAGAGATCAGATGTTCCCATCAGAA 1621

DB 163 -----AspGlnArgPheProSerGlu 169

QY 1622 TCCAAACGACAGAGATGAGATATTCTTGGGATCTCTGGGAGTCTCTTTCAGAGTTCT 1681

DB 170 SerLysGlnGluAspGluGluThrSerCysAspSerArgSerLeuPheGluSerSer 189

QY 1682 GCAAAAGTCAAGTGTGTACCTGAGTCTATGATCAGAAAGATGATGAGATAAATAGA 1741

DB 190 AlaLysIleGlnValCysIleProGluSerIleTyrGlnLysValMetGluIleAsnArg 209

QY 1742 GAAGTAGAAGAGCTTCTGAGAGCCATCTGCCTCAAGCCCTGCCGTGAAATGCAAAAG 1801

DB 210 GluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGlnAsn 229

QY 1802 ACTGTTCCAAATTAAGCCTTTGAATTTGAAGATGAACAAACATTTGAGAGCAGCTCAGATG 1861

DB 230 SerValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAspProMet 249

QY 1862 TTCCCATCAGAATCCAAACAAAGGACGATGAAGAAAATTTCTTGGGATTTCTGAGATCCC 1921

DB 250 PheProProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSerLeu 269

QY 1922 TGTGAGACGGTTTTCACAGAGGATGTGATTTTACCACCAAGCTACATCAAAAGAAATTC 1981

DB 270 CysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIle 289

QY 1982 GATACCTTAAGTGGAAAATTAAGAGAGTCTCTCTGTTAAAGATGCTCTTCTGAAGCCTACC 2041

DB 290 AspLysIleAsnGlnLysLeuGluGluSerProAsnLysAspGlyLeuLeuLysAlaThr 309

QY 2042 TGTGGAAGGAAAGTTCTCTTCCAAATTAAGCCTTAGAATTAAGGACAGAGAAACATTC 2101

DB 310 CysGlyMetLysValSerIleProThrLysAlaLeuGluLeuLysAspMetGlnThrPhe 329

QY 2102 AAGCACAGTCTCTGTATTAAGATGGTCTTCTGAAGCCTACCTGTGGAAGAAAGTTTCT 2161

DB 330 LysAlaGluProProGlyLysProSerAlaPheGluProAlaThrGluMetGlnLysSer 349

QY 2162 CTTCCAAATTAAGCCTTAGAATTAAGGACAGAGAAACACTCAAGACAGAGTCTCTGAT 2221

DB 350 ValProAsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAsp-----366

QY 2222 AATGATGCTCTTCTGAAGCCTACCTGTGGAAGAAAGTTTCTCTTCCAAATAAGCTTTA 2281

DB 366 -----366

QY 2282 GAATTGAAGGACAGAGAAACATTCAAAGAGCTCAGATGTTCCCATCAGATCCAAACAA 2341

DB 367 -----GluIleLeuProSerGluSerLysGln 375

QY 2342 AAGATGATGAAGAAATTTCTTGGATTTTGAAGTTTCTTTCAGACTCTCTTACAGAT 2401

DB 376 LysAspTyrGluGluSerTrpAspSerGluSerLeuCysGluThrValSerGlnLys 395

QY 2402 GATGTGTTTACCAGGCTACACATCAAAAAGAAATTCGATACCTTAAGTGAAGAAATTA 2461

DB 396 AspValCysLeuProLysAla\*\*HisGlnLysGluIleAspLysIleAsnGlyLysLeu 415

QY 2462 GAAGAGTCTCTGTATAAGATGTGTTCTGAAGCCTACCTGTGGAATGAAATTTCTCTT 2521

DB 416 GluglySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIle 435

QY 2522 CCAATTAAGCCTTAGAATTAAGGACAGAGAAACATTCAAAGACAGAGGATGTGAGTTCT 2581

DB 436 ProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLys 455

QY 2582 GTAGAGTCCCATTCAGTCTTTTGGCAACCCAGTACTGAAAATTCACAGTCTCAAAA 2641

DB 456 ---ProSerAlaPhe-----GluProAlaIleGluMetGlnLysSerVal---469

QY 2642 GTTCAGGAAGACTTTAATCTTACTACCAAGGAGGACAAAGACAGTAACTGGACAA 2701

DB 470 -----ProAsnLysAlaLeuGluLeuLys 477

QY 2702 CAGGAAGCTGATATTGGCATTATTGAACGAGCTCCACAGATCAAAACAATAAGATGCC 2761

DB 478 AsnGluGlnThrLeuArgAlaAspGluIleLeuPro-----489

QY 2762 ACATCAGAATTAGGAAGAAAGAGATACAAATCAACTTCAGATTTCTGAGATTATCTCT 2821

DB 490 ---SerGluSerLysGlnLysAspTyrGluGluSerTrpAspSerGluSerLeuCys 508

QY 2822 GTGAGTGCATACACAGAAATTTAGTGTTTACCTCAGGCTACATATCAAAAGAAATAAAG 2881

DB 509 GluThrValSerGlnLysAspValCysLeuProLysAla\*\*HisGlnLysGluIleAsp 528

QY 2882 ACAACAAATGGCAAAATAGAGAGTCT-----2908

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Db 529 LysIleAsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCys 548
QY 2908 -----
Db 549 ArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLys 568
QY 2909 -----CCTGAAAGCCTTCTCAGCTTGTAGCCTGCGCACTGAAATGCAAACTCTCTTT 2959
Db 569 AlaGluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerVal 588
QY 2960 CCAATTAAGGCTTGAATGGAAGATAAACAACATTGAGAGCA----- 3004
Db 589 ProAsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGlnMetPhePro 608
QY 3004 ----- 3004
Db 609 SerGluSerLysGlnLys**ValGluGluAsnSerTrpAspSerGluSerLeuArgGlu 628
QY 3004 ----- 3004
Db 629 ThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLys 648
QY 3005 -----GATTCACCTACCTATCAAAATCTTGGATGCGCTTCTTCT 3046
Db 649 IleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSer 668
QY 3047 TGTGAAGAGGAGGAACTTAAAGATAACTGTGAACAAATTCACAGCAAAATGGAA 3106
Db 669 CysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGlu 688
QY 3107 CAATGMAAAATAGTTTGTCTACTACAAAGAGAACTGTCAAGACCAAGAAATATAA 3166
Db 689 GlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGlnLys 708
QY 3167 TCACAGTTAGAGAACCAAAAGCTAAATGGGAACAGAGCTCTGCAGTGTGAGATTGGCT 3226
Db 709 SerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThr 728
QY 3227 TTAATCAAGAGAGAGAGAGAGAAATGTCGATATATTAAGAAAGAAATAGACCC 3286
Db 729 LeuAsnGlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGlu 748
QY 3287 -----GAACAGCAACTTAGGAAAAGTTAGAGTGAACACCACTGAA 3331
Db 749 GluLeuGlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnLeuGlu 768
QY 3332 CAGACTCTCAGATACAGATATAGAAATGAAAGCTGTAAACAGTAATTTGAATCAGTT 3391
Db 769 GlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnVal 788
QY 3392 TCTCAGACTCATGAAGTCAAAATGATCTCTTTCATGAAATTCGATGTTGAAAGGAA 3451
Db 789 SerHisThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysGlu 808
QY 3452 ATTGCCATCTAAACTGGAAGTACGACACTGAAACATCAACACAGCTGAAGGAAAT 3511
Db 809 IleAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTrpGlnGluLysGluAsn 828
QY 3512 AAATCTTTGAGACATTAAGATTTTACAAGAAAGATGCTGAATCTCAATGACCTTA 3571
Db 829 LysTyPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeu 848
QY 3572 AAATCAAAACAGAAACAGTAAACAAAGGCGATCTCAGTATAGAGAGCAGCTTAAAGTT 3631
Db 849 LysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysVal 868
QY 3632 CTGACGGCAGAGAACAGTGTGACTTCTAAATTGAAGGAA 3673
Db 869 LeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 882
RESULT 13
AAU33351
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ID XX AAU33351 standard; protein; 1002 AA.
AC XX AAU33351;
DT 18-DEC-2001 (first entry)
DE Human breast cancer protein B726P from alternatively spliced cDNA.
KW Human; ss; breast cancer protein; tumour; cancer; cytostatic;
KW gene therapy; immunogen.
XX Homo sapiens.
XX WO200179286-A2.
XX 25-OCT-2001.
XX 12-APR-2001; 2001WO-US012164.
XX 17-APR-2000; 2000US-00551621.
XX 08-JUN-2000; 2000US-00590751.
XX 22-JUN-2000; 2000US-00604287.
XX 20-JUL-2000; 2000US-00620405.
XX (CORI-) CORIXA CORP.
XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
PI WPI; 2001-611721/70.
XX N-PSDB; AAS47411.
DR Breast Tumor Proteins and nucleic acids useful for the prevention,
XX diagnosis and treatment of breast cancer.
XX Claim 3; Page 281-283; 297pp; English.
XX The invention relates to isolated breast tumour proteins and nucleic
XX acids that encode them, including immunogenic fragments of the proteins.
XX Also included are expression vectors expressing the proteins, transformed
XX cells and antibodies raised against the proteins or an antigen presenting
XX cell expressing the protein. The proteins and nucleic acids may be used
XX in the prevention, diagnosis and treatment of diseases associated with
XX inappropriate breast tumour protein expression, i.e. breast tumours and
XX breast cancer e.g by gene therapy. The nucleic acids and their
XX complements may also be used as DNA probes in diagnostic assays to detect
XX and quantitate the presence of similar nucleic acids in samples, and
XX therefore which patients may be in need of restorative therapy. The
XX proteins, nucleic acids and antibodies may be used in assays to identify
XX modulators (e.g. antagonists) of breast tumour protein expression and
XX activity. The antibodies and antagonists may also be used to down
XX regulate expression and activity. The antibodies may also be used as
XX diagnostic agents for detecting the presence of the proteins in samples
XX (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immuno-
XX purification diagnostic techniques. The present sequence is a breast
XX tumour protein encoded by a cDNA from a breast tumour cDNA library
XX isolated by subtractive hybridisation against a normal breast cDNA
XX library
SQ Sequence 1002 AA;
Alignment Scores:
Pred. No.: 3.19e-184 Length: 1002
Score: 2367.00 Matches: 511
Percent Similarity: 62.62% Conservative: 62
Best Local Similarity: 55.85% Mismatches: 126
Query Match: 36.71% Indels: 216
DB: 4 Gaps: 9
US-09-602-362E-26 (1-3673) x AAU33351 (1-1002)
QY 1199 TTGAGGCTCAAAAGAAACATCTGAGAAATTTTCATGGCCAGCAAAAGAAATCTAGG 1258
Db 1 MetSerProAlaLysGluThrSerGluLysPheThrAlaLysGlyArgProArg 20
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QY 1859 ATGTTCCCATCAGAAATCCAAACAAAGGAGGATGAGAAATTTCTTGGGATTCAGACT 1918  
 Db |||||  
 QY 1919 CCCTGTGAGAGGTTTACAGAGGATGTGTATTTACCCAAAGCTACACATCAAAAGAA 1978  
 Db |||||  
 QY 1979 TTCGATACCTTAAGTGGAAATTAGAGAGCTCTCTGTTAAAGATGGTCTTCTGAGCCT 2038  
 Db |||||  
 QY 2039 ACCTGTGGAAGAAAGTTTCTCTTCCAAATAAAGCCTTAGAAATTAAGACAGAGAAACA 2098  
 Db |||||  
 QY 2159 TCTCTTCCAAATTAAGCCTTAGAATTAAGGACAGAGAAACACTCAAGCAGAGCTCTCT 2218  
 Db |||||  
 QY 2219 GATAATGATGCTTCTGAGCCTACTCTGTGAAGGAAAGTTTCTCTTCCAAATAAAGCT 2278  
 Db |||||  
 QY 2279 TTAGAATTGAAGGACAGAGAAACATTCAGAGCCTCAGATGTTCCCATCAGATCCCAA 2338  
 Db |||||  
 QY 2339 CAAAGGATGATGAAGAAATTTCTGGGATTTTGAGAGTTTCTCTGAGACTCTCTACAG 2398  
 Db |||||  
 QY 2399 AATGATGCTGTATCCAGGCTACACATCAAAAGAAATTCGATACCTTAAGTGGAA 2458  
 Db |||||  
 QY 2459 TTAGAGAGCTCTCCTGATTAAGATGCTTCTTCAAGCCTACTACCTGTGGAATGAAATTTCT 2518  
 Db |||||  
 QY 2519 CTTCGAATTAAGCCTTAGAATTAAGGACAGAGAAACATTCAGAGCAGAGATGTGAGT 2578  
 Db |||||  
 QY 2579 TCTGTAGAGTCCACATTCAGTCTTTTGGCAACCGACTACTGTGAAATTCAGTCTACA 2638  
 Db |||||  
 QY 2639 AAGTTGAGGAAGCTTTAATCTTACTACAGGAGGAGCAACAGACAGACTACTCGA 2698  
 Db |||||  
 QY 2699 CAACGAGACGATGATTTGGCATTATTGAACGAGCTCCACAGATCAACAAATTAAGATG 2758  
 Db |||||  
 QY 2759 CCCACATCAGAATTAAGGAAAGAGATCAAAATCAACTTCAGATTTCTGAGATTATC 2818  
 Db |||||  
 QY 2819 TCTGTGAGTACACAGATTAATGATGTTTACTCTGAGCTACATATCAAAAGAAATA 2878  
 Db |||||  
 QY 2879 AAGACAAACAAATGCAAGAGTCT 2908  
 Db |||||  
 QY 435 AspLysIleAsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaPro 454

QY 2908 ----- 2908  
 Db CysArgMetLysValSerIleProThrLysAlaLeuLeuMetAspMetGlnThrPhe 474  
 QY 2909 -----CCTGAAAGCCTTCTCCTTTGAGCTGCCACTGAAATGCAAACTCT 2956  
 Db |||||  
 QY 475 LysAlaGluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSer 494  
 QY 2957 GTTCCAAATAAGCCTTAGAATGGAAGAAATAACAAACATTCGAGACA----- 3004  
 Db |||||  
 QY 495 ValProAsnLysAlaLeuGluLeuLysAsnGlnThrLeuArgAlaAspGlnMetPhe 514  
 QY 3004 ----- 3004  
 Db 515 ProSerGluSerLysGlnLys\*\*\*ValGluLysAsnSerTrpAspSerGluSerLeuArg 534  
 QY 3004 ----- 3004  
 Db 535 GluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAsp 554  
 QY 3005 -----GATTCAACTACCTATCAAAATCTTGGATGCACCTCTCT 3043  
 Db |||||  
 QY 555 LysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHis 574  
 QY 3044 TCTTGTGAAAGAGGAACTTTAAAGAAAGATACTGTGAACAAATTCAGCAAAATG 3103  
 Db |||||  
 QY 575 SerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMet 594  
 QY 3104 GAACAAATGAAATTAAGTTTGTGTACTACAAAGGAACTGTCAAGCGAAGAAATA 3163  
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 QY 595 GluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIle 614  
 QY 3164 AAATCAGATTTAGAGAACCAAAAGCTAAATGGGAAACAGAGCTCTGCAGTGTGAGATTG 3223  
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 QY 615 LysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLysCysSerValArgLeu 634  
 QY 3224 CCTTTAATCAAGAGAGAGAGAGAGAAATTCGTATATATATAAGAAATAATG 3283  
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 QY 635 ThrLeuAsnGlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArg 654  
 QY 3284 CCC-----GAAGAGCACTTAGGAAAGTTAGAACTGAAACACCAACTT 3328  
 Db |||||  
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 QY 3329 GACAGACTCTCAGATACAGATATAGAAATGAAAAGTGTAAACAGTAATTTGATCAG 3388  
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 QY 3389 GTTCTCACACTCATGAAAGTGAATGATCTCTTTCAAGAAATTCATGTTGAAAAAG 3448  
 Db |||||  
 QY 695 ValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLys 714  
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 QY 715 GluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGlu 734  
 QY 3509 AATAATATCTTTCAGGACATTAAGATTTTACAGAAAGAAATGCTGAATCTCAATGACC 3568  
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 QY 735 AsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThr 754  
 QY 3569 CTAAGACTGAACAGAAAAACAGTAACAAAAAGGCATCTCAGTATAGAGAGCAGCTTAA 3628  
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 QY 755 LeuLysLeuLysGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLys 774  
 QY 3629 GTTCTCAGCGCAGAGACAGGATGCTGACTTCTAAATTCAGAGAA 3673  
 Db |||||  
 QY 775 ValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGlu 789

RESULT 15  
 ABJ37741 standard; protein; 1002 AA.  
 ID ABJ37741  
 XX  
 AC ABJ37741;



